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| (54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides. | | |

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COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 μ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 μ l of H₂O, heat-denatured and mixed with 100 μ l (100 μ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 μ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μ l H₂O to form the driver DNA.

To form the tracer DNA, 10 μ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 μ l H₂O. Tracer DNA was mixed with 15 μ l driver DNA and 20 μ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μ l H₂O, mixed with 8 μ l driver DNA and 20 μ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

Example 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun
Dillin, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.427C3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC      60
ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACCTC CCCCATAGT GAATCAGCTT      120
CCAGGGGGTC CAGTCCCTCT CCTTACTTCA TCCCACATCC ATGCCAAAGG AAGACCTTCC      180
CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCCCT CAGGACAGAG TGGGTTATGT      240
TTTCAGCTCC ATCCTTGCTG TGAGTGTCTG GTGCGTTGTG CCTCCAGCTT CTGCTCAGTG      300
CTTCATGGAC AGTGTCAGC ACATGTCACT CTCCACTCTC TCAGTGTGGA TCCACTAGTT      360
CTAGAGCGGC CGCCACCGCG GTGGAGCTCC AGCTTTTGTT CCCTTTAGTG AGGGTTAATT      420
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| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGCGCTTGG | CGTAATCATG | GTCATAACTG | TTTCCTGTGT | GAAATTGTTA | TCCGCTCACA | 480 |
| ATTCCACACA | ACATACGAGC | CGGAAGCATA | AAGTGTAAG | CCTGGGGTGC | CTAATGAGTG | 540 |
| ANCTAACTCA | CATTAATTGC | GTTGCGCTCA | CTGNCCGCTT | TCCAGTCNGG | AAAAGTGTGC | 600 |
| TGCCAGCTGC | ATTAATGAAT | CGGCCAACGC | NCGGGGAAAA | GCGGTTTGCG | TTTGGGGGCG | 660 |
| TCTTCCGCTT | CTCGCTCACT | NANTCCTGCG | CTCGGTCNTT | CGGCTGCGGG | GAACGGTATC | 720 |
| ACTCCTCAAA | GGNGGTATTA | CGGTTATCCN | NAAATCNGGG | GATACCCNGG | AAAAAANTTT | 780 |
| AACAAAAGGG | CANCAAAGGG | CNGAAACGTA | AAAA | | | 814 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| ACAGAAATGT | TGGATGGTGG | AGCACCTTTC | TATACGACTT | ACAGGACAGC | AGATGGGGAA | 60 |
| TTCATGGCTG | TTGGAGCAAT | AGAACCCAG | TTCTACGAGC | TGCTGATCAA | AGGACTTGGA | 120 |
| CTAAAGTCTG | ATGAACCTCC | CAATCAGATG | AGCATGGATG | ATTGGCCAGA | AATGAAGAAG | 180 |
| AAGTTTGCAG | ATGTATTTGC | AAAGAAGACG | AAGGCAGAGT | GGTGTCAAAT | CTTTGACGGC | 240 |
| ACAGATGCCT | GTGTGACTCC | GGTTCTGACT | TTTGAGGAGG | TTGTTTCATCA | TGATCACAAAC | 300 |
| AAGGAACGGG | GCTCGTTTAT | CACCACTGAG | GAGCAGGACG | TGAGCCCCCG | CCCTGCACCT | 360 |
| CTGCTGTTAA | ACACCCAGC | CATCCCTTCT | TTCAAAAGGG | ATCCACTAGT | TCTAGAAGCG | 420 |
| GCCGCCACCG | CGGTGGAGCT | CCAGCTTTTG | TTCCCTTTAG | TGAGGGTTAA | TTGCGCGCTT | 480 |
| GGCGTAATCA | TGGTCATAGC | TGTTTCCTGT | GTGAAATTGT | TATCCGCTCA | CAATTCCCCC | 540 |
| AACATACGAG | CCGGAACATA | AAGTGTTAAG | CCTGGGGTGC | CTAATGANTG | AGCTAACTCN | 600 |
| CATTAATTCG | GTTGCGCTCA | CTGCCCGCTT | TCCAGTCGGG | AAAAGTGTGC | TGCCACTGCN | 660 |
| TTANTGAATC | NGCCACCCCC | CGGGAAAAGG | CGGTTGCNTT | TTGGGCCTCT | TCCGCTTTCC | 720 |
| TCGCTCATTC | ATCCTNGCNC | CCGGTCTTCG | GCTGCGNGA | ACGGTTCACT | CCTCAAAGGC | 780 |
| GGTNTNCCGG | TTATCCCCAA | ACNGGGGATA | CCNGA | | | 816 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTTTGAAAG | AAGGGATGGC | TGGGGTGTTT | AACAGCAGAG | GTGCAGGGCG | GGGGCTCACC | 60 |
| TCCTGCTCCT | CACTGGTGAT | AAACGAGCCC | CGTTCCTTGT | TGTGATCATG | ATGAACAACC | 120 |
| TCCTCAAAG | TCAGAACCGG | AGTCACACAG | GCATCTGTGC | CGTCAAAGAT | TTGACACCAC | 180 |
| TCTGCCCTTC | TCTTCTTTGC | AAATACATCT | GCAAACCTCT | TCTTCATTTT | TGGCCAATCA | 240 |
| TCCATGCTCA | TCTGATTGGG | AAGTTCATCA | GACTTTAGTC | CANNTCCTTT | GATCAGCAGC | 300 |
| TCGTAGAACT | GGGGTTCTAT | TGCTCCAACA | GCCATGAATT | CCCCATCTGC | TGTCCTGTAA | 360 |
| GTCGTATAGA | AAGGTGCTCC | ACCATCCAAC | ATGTTCTGTC | CTCGAGGGGG | GGCCCGGTAC | 420 |
| CCAATTCGCC | CTATANTGAG | TCGTATTACG | CGCGCTCACT | GGCCGTCGTT | TTACAACGTC | 480 |
| GTGACTGGGA | AAACCCCTGG | CGTTACCAAC | TTAATCGCCT | TGCAGCACAT | CCCCCTTTTC | 540 |
| CCAGCTGGGC | GTAATANCAG | AAAGGCCCGC | ACCGATCGCC | CTTCCAACAG | TTGCGCACCT | 600 |
| GAATGGGNAA | ATGGGACCCC | CCTGTTACCG | CGCATTNAAC | CCCCGCNNGG | TTTNGTTGTT | 660 |
| ACCCCCACNT | NNACCGCTTA | CACTTTGCCA | GCGCCTTANC | GCCCCGCTCC | TTTCNCCTTT | 720 |
| CTTCCCTTCC | TTTCNCNCCN | CTTTCCTCCG | GGGTTTCCCC | CNTCAAACCC | CNA | 773 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCTCCTGAGT CCTACTGACC TGTGCTTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG      60
AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTT CTCCTCTCCT      120
TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG      180
ACGTGGGTGA CCATGTTGTT TGTGGGGTGC AGAGATGGGA GGGGTGGGGC CCACCCCTGGA      240
AGAGTGGACA GTGACACAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC      300
ACAAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCCT      360
GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAAG AAGGGGAGGA TCCACTAGTT      420
CTANAGCGCG CGCCACCGCG GTGGANCTCC ANCTTTTGT CCCTTTAGTG AGGGTTAATT      480
GCGCGCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA      540
ATTCCACACA ACATACGANC CGGAAACATA AANTGTAAAC CTGGGGTGCC TAATGANTGA      600
CTAACTCACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAATCNGGAA ACCTGTCTTG      660
CCNCTTGCAT TNATGAATCN GCCAACCCCC GGGGAAAAGC GTTTGCGTTT TGGGCGCTCT      720
TCCGCTTCCT CNCTCANTTA NTCCCTNCNC TCGGTCATTC CGGCTGCNGC AAACCGGTTT      780
ACCNCCTCCA AAGGGGGTAT TCCGGTTTCC CCNAATCCG GGANANNC      828

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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TTTTTTTTTT TTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT      60
AGTTTAAATT GCATCCAAAG TACTAACAAA AACTCTAGCA ATCAAGAATG GCAGCATGTT      120
ATTTTATAAC AATCAACACC TGTGGCTTTT AAAATTGGT TTTCATAAGA TAATTTATAC      180
TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTTAGGT CACTCCAAGC TTGGCAGTTA      240
ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTTAAT AAATAACAAA TACAACATTG      300
TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG      360
AATAGAATAC CTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTAC TCAGCCCTGA      420
CATTGAGTTT TCAAAGTAGG AGACAGGTTT TACAGTATCA TTTACAGTT TCCAACACAT      480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA      540
TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC      600
TTATTTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT      660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTTGA ACTGGAACAT      720
TGNATNACAG TGTTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA      780
TGTTATTTTG TTAATAATTA AATTTTAACC TGGTGGAAAA ATAATTGAA ATNA      834

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA      60
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TGTAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT      180
GACGTGAAGT CCGTGGAAGC CTGTGGCTAC AAAAAATGTT GAGCCGTAGA TGCCGTCGGA      240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAAG AGGGTAAAT AGAGACCCAG      300
TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG      360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC      420
TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCCTA GTTGGGGGGT      480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA      540
GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC      600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTGGG      660
TTANTANGGC CTANTATGAA GAACCTTTGG ANTGGAATTA AATCAATNGC TTGGCCGGAA      720
GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTTA CCCNACCCAT      780
GGAATNCNCC CCGGACNA NTGNATCCCT ATCTTAA      818

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA      60
CGGGCCCTAT TTCAAAGATT TTTAGGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT      120
GGTTTGCTCC ACAGATTTC AAGCATTGAC CGTAGTATAC CCCCAGTCGT GTAGCGGTGA      180
AAGTGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG      240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGGCT TCAATCGGGA      300
GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG      360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC      420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT TGAACCTCGT TGTTATGTAA      480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTIONGA TNAATGGCGG GCANGATATT      540
TCAAACNGTC TCTANTTCCT GAAACGCTG AAATGTTAAT AANAATTAA TTTNGTTATT      600
GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG      660
CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCCACNCNN      720
ACNATTGGAT NCCCCANTTC CANAAANGGC NCCCCCCGG TGNANNCCNC CTTTGTGTTCC      780
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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG      60
CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA TCCGAGCGT      120

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGAAGCGCA | CGTCCCAGAA | GGTGGACTTG | GCACTGAAAC | AGCTGGGACA | CATCCGCGAG | 180 |
| TACGAACAGC | GCCTGAAAGT | GCTGGAGCGG | GAGGTCCAGC | AGTGTAGCCG | CGTCCTGGGG | 240 |
| TGGGTGGCCG | ANGCCTGANC | CGCTCTGCCT | TGCTGCCCCC | ANGTGGGCCG | CCACCCCTG | 300 |
| ACCTGCCTGG | GTCCAAACAC | TGAGCCCTGC | TGGCGGACTT | CAAGGANAAC | CCCCACANGG | 360 |
| GGATTTTGCT | CCTANANTAA | GGCTCATCTG | GGCTCGGCC | CCCCACCTG | GTGGCCTTG | 420 |
| TCTTTGANGT | GAGCCCCATG | TCCATCTGGG | CCACTGTCNG | GACCACCTTT | NGGGAGTGTT | 480 |
| CTCCTTACAA | CCACANNATG | CCCGGCTCCT | CCCGGAAACC | ANTCCCANCC | TGNGAAGGAT | 540 |
| CAAGNCCTGN | ATCCACTNNT | NCTANAACCG | GCCNCCNCCG | CNGTGGAACC | CNCCTTNTGT | 600 |
| TCCTTTTCNT | TNAGGGTTAA | TNNCGCCTTG | GCCTTNCCAN | NGTCCTNCNC | NTTTTCCNNT | 660 |
| GTTNAAATTG | TTANGCNCCC | NCCNNTCCCN | CNNCNCNAN | CCCGACCCNN | ANNTTNANN | 720 |
| NCCTGGGGGT | NCCNCCNGAT | TGACCCNCC | NCCCTNTANT | TGCNTTNGGG | NNCNTGCC | 780 |
| CTTCCCTCT | NGGGANNCG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACGCCTTGAT | CCTCCCAGGC | TGGGACTGGT | TCTGGGAGGA | GCCGGGCATG | CTGTGGTTTG | 60 |
| TAANGATGAC | ACTCCCAAAG | GTGGTCCTGA | CAGTGGGCCA | GATGGACATG | GGGCTCACCT | 120 |
| CAAGGACAAG | GCCACCAGGT | GCGGGGGCCG | AAGCCACAT | GATCCTTACT | CTATGAGCAA | 180 |
| AATCCCCTGT | GGGGGCTTCT | CCTTGAAGTC | CGCCANCAGG | GCTCAGTCTT | TGGACCCANG | 240 |
| CAGGTCAATG | GGTTGTNGNC | CAACTGGGGG | CCNCAACGCA | AAANGGCNCA | GGGCCTCNGN | 300 |
| CACCCATCCC | ANGACGCGGC | TACACTNCTG | GACCTCCNC | TCCACCACTT | TCATGCGCTG | 360 |
| TTCNTACCCG | CGNATNTGTC | CCANCTGTTT | CNGTGCCNAC | TCCANCTTCT | NGGACGTGCG | 420 |
| CTACATACGC | CCGGANTCNC | NCTCCCGCTT | TGTCCCTATC | CACGTNCCAN | CAACAAATTT | 480 |
| CNCCNTANTG | CACCNATTC | CACNTTTNNC | AGNTTTCCNC | MNCGNGCTTC | CTTNTAAAAG | 540 |
| GGTTGANCCC | CGGAAAATNC | CCCAAAGGGG | GGGGGCCNGG | TACCCAAC | TTCTNAACTT | 600 |
| GCTGAANTCC | CCATNACCNN | GNCTCNATGG | ANCCNTCCNT | TTTAANNACN | TTCTNAACTT | 660 |
| GGGAANANCC | CTCGNCCNTN | CCCCCNTTAA | TCCNCCTTG | CNANGNCCNT | CCCCCNNTCC | 720 |
| NCCCNNTNG | GCNTNTNANN | CNAAAAGGC | CCMNNANCA | TCTCCTNNCN | CCTCANTTCG | 780 |
| CCANCCCTCG | AAATCGGCCN | C | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CAGTCTATNT | GGCCAGTGTG | GCAGCTTTCC | CTGTGGCTGC | CGGTGCCACA | TGCCTGTCCC | 60 |
| ACAGTGTGGC | CGTGGTGACA | GCTTCAGCCG | CCCTCACC | GTTTCACTTC | TCAGCCCTGC | 120 |
| AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | GAAGCAGGTG | TTCTGCCCCA | 180 |
| AATACCGAGG | GGACACTGGA | GGTGTAGCA | GTGAGGACAG | CCTGATGACC | AGCTTCCTGC | 240 |
| CAGGCCCTAA | GCCTGGAGCT | CCCTCCCTA | ATGGACACGT | GGGTGCTGGA | GGCAGTGGCC | 300 |
| TGCTCCCACC | TCCACCCGCG | CTCTGCGGGG | CCTCTGCTG | TGATGTCTCC | GTACGTGTGG | 360 |
| TGGTGGGTGA | GCCACCGAN | GCCAGGGTGG | TTCGGGCCG | GGGCATCTGC | CTGGACCTCG | 420 |
| CCATCCTGGA | TAGTGCTTCC | TGCTGTCCCA | NGTGCCCCA | TCCCTGTTTA | TGGGCTCCAT | 480 |
| TGTCCAGCTC | AGCCAGTCTG | TCACTGCCTA | TATGGTGTCT | GCCGCAGGCC | TGGGTCTGGT | 540 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCCATTACT | TTGCTACACA | GGTANTATTT | GACAAGAACG | ANTTGGCCAA | ATACTCAGCG | 600 |
| TTAAAAAATT | CCAGCAACAT | TGGGGGTGGA | AGGCCTGCCT | CACTGGGTCC | AACTCCCCGC | 660 |
| TCCTGTAAAC | CCCATGGGGC | TGCCGGCTTG | GCCGCCAATT | TCTGTTGCTG | CCAAANTNAT | 720 |
| GTGGCTCTCT | GCTGCCACCT | GTTGCTGGCT | GAAGTGCNTA | CNGCNCANCT | NGGGGGGTNG | 780 |
| GGNGTTCCC | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| CCCCCCTAC | CCAAATATTA | GACACCAACA | CAGAAAAGCT | AGCAATGGAT | TCCCTTCTAC | 60 |
| TTTGTTAAAT | AAATAAGTTA | AATATTTAAA | TGCCTGTGTC | TCTGTGATGG | CAACAGAAGG | 120 |
| ACCAACAGGC | CACATCCTGA | TAAAAGGTAA | GAGGGGGGTG | GATCAGCAAA | AAGACAGTGC | 180 |
| TGTGGGCTGA | GGGGACCTGG | TTCTTGTGTG | TTGCCCCCTCA | GGACTCTTCC | CCTACAAATA | 240 |
| ACTTTCATAT | GTTCAAATCC | CATGGAGGAG | TGTTTCATCC | TAGAAACTCC | CATGCAAGAG | 300 |
| CTACATTAAA | CGAAGCTGCA | GGTTAAGGGG | CTTANAGATG | GGAAACCAGG | TGACTGAGTT | 360 |
| TATTGAGCTC | CAAAAACCC | TTCTCTAGGT | GTGTCTCAAC | TAGGAGGCTA | GCTGTTAACC | 420 |
| CTGAGCCTGG | GTAATCCACC | TGCAGAGTCC | CCGCATTCCA | GTGCATGGAA | CCCTTCTGGC | 480 |
| CTCCCTGTAT | AAGTCCAGAC | TGAAACCCCC | TTGGAAGGNC | TCCAGTCAGG | CAGCCCTANA | 540 |
| AACTGGGGAA | AAAAGAAAAG | GACGCCCCAN | CCCCCAGCTG | TGCANCTACG | CACCTCAACA | 600 |
| GCACAGGGTG | GCAGCAAAAA | AACCACTTTA | CTTGGGCACA | AACAAAAACT | NGGGGGGGCA | 660 |
| ACCCCGGCAC | CCCNANGGGG | GTTAACAGGA | ANCNGGGNAA | CNTGGAACCC | AATTNAGGCA | 720 |
| GGCCCNCCAC | CCCNAAATNTT | GCTGGGAAAT | TTTTCTCTCC | CTAAATTNTT | TC | 772 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GCCCCAATTC | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCCCTC | TACTTTTTTG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT | GTCAATTGCA | CAGAATGGGG | GAAAGGCACT | GTTCTCTTTG | 180 |
| AAGTANGGTG | AGTCCTCAAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGGTGT | TCCCACTTGT | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GGAAGTGCTC | AGCCATTGTG | GTGTACACCA | AGGCGACCAC | 360 |
| AGCAGCTGCN | ACCTCAGCAA | TGAAGATGAN | GAGGANGATG | AAGAAGAACG | TCNCGAGGGC | 420 |
| ACACTTGCTC | TCAGTCTTAN | CACCATANCA | GCCCNTGAAA | ACCAANANCA | AAGACCACNA | 480 |
| CNCCGGCTGC | GATGAAGAAA | TNACCCCNCG | TTGACAAACT | TGCATGGCAC | TGGGANCCAC | 540 |
| AGTGGCCNNA | AAAATCTTCA | AAAAGGATGC | CCCATCNATT | GACCCCCCAA | ATGCCCACTG | 600 |
| CCAACAGGGG | CTGCCCCACN | CNCNNAACGA | TGANCCNATT | GNACAAGATC | TNCNTGGTCT | 660 |
| TNATNAACNT | GAACCCTGCN | TNGTGGCTCC | TGTTCAAGNC | CNNGGCCTGA | CTTCTNAANN | 720 |
| AANGAACTCN | GAAGNCCCCA | CNGGANANNC | G | | | 751 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGCCAGGCG | TCCCTCTGCC | TGCCCCTCA | GTGGCAACAC | CCGGGAGCTG | TTTTGTCCTT | 60 |
| TGTGGANCCT | CAGCAGTNCC | CTCTTTCAGA | ACTCANTGCC | AAGANCCCTG | AACAGGAGCC | 120 |
| ACCATGCAGT | GCTTCAGCTT | CATTAAGACC | ATGATGATCC | TCTTCAATT | GCTCATCTTT | 180 |
| CTGTGTGGTG | CAGCCCTGTT | GGCAGTGGG | ATCTGGGTGT | CAATCGATGG | GGCATCCTTT | 240 |
| CTGAAGATCT | TCGGGCCACT | GTCTCCAGT | GCCATGCAGT | TTGTCAACGT | GGGCTACTTC | 300 |
| CTCATCGCAG | CCGGCGTTGT | GGTCTTAGCT | CTAGGTTTCC | TGGGCTGCTA | TGGTGCTAAG | 360 |
| ACTGAGAGCA | AGTGTGCCCT | CGTGACGTT | TTCTTCATCC | TCCTCCTCAT | CTTCATTGCT | 420 |
| GAGGTTGCAA | TGCTGTGGTC | GCCTTGGTGT | ACACCACAAT | GGCTGAGCAC | TTCTGACGCT | 480 |
| TGCTGGTAAT | GCCTGCCATC | AANAAAAGAT | TATGGGTTC | CAGGAANACT | TCACTCAAGT | 540 |
| GTTGGAACAC | CACCATGAAA | GGGCTCAAGT | GCTGTGGCTT | CNNCCAATA | TACGGATTTT | 600 |
| GAAGANTCAC | CTACTTCAAA | GAAAANAGTG | CCTTCCCCC | ATTCTGTTG | CAATTGACAA | 660 |
| ACGTCCCCAA | CACAGCCAAT | TGAAAACCTG | CACCCAACCC | AAANGGTCC | CCAACCANAA | 720 |
| ATTNAAGGG | | | | | | 729 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| TGCTCTTCT | CAAAGTTGTT | CTTGTGCCA | TAACAACCAC | CATAGGTAAA | GCGGGCGCAG | 60 |
| TGTTTCGCTGA | AGGGGTTGTA | GTACCAGCGC | GGGATGCTCT | CCTTGACAGAG | TCCTGTGTCT | 120 |
| GGCAGGTCCA | CGCAGTGCCC | TTTGTCAGT | GGGAAATGGA | TGCGCTGGAG | CTCGTCAAAG | 180 |
| CCACTCGTGT | ATTTTTCACA | GGCAGCCTCG | TCCGACGCGT | CGGGGCAGTT | GGGGGTGTCT | 240 |
| TCACACTCCA | GGAACTGTC | NATGCAGCAG | CCATTGCTGC | AGCGGAACAG | GGTGGGCTGA | 300 |
| CANGTGCCAG | AGCACACTGG | ATGGCGCCTT | TCCATGNNAN | GGGCCCTGNG | GGAAAGTCCC | 360 |
| TGANCCCCAN | ANCTGCCTCT | CAAANGCCCC | ACCTTGACACA | CCCCGACAGG | CTAGAATGGA | 420 |
| ATCTTCTTCC | CGAAAGGTAG | TTNTTCTTGT | TGCCCAANCC | ANCCCCNTAA | ACAAACTCTT | 480 |
| GCANATCTGC | TCCGNGGGGG | TCNTANTACC | ANCGTGGGAA | AAGAACCCCA | GGCNGCGAAC | 540 |
| CAANCTTGTT | TGGATNCGAA | GCNATAATCT | NTNTTCTG | TTGGTGGACA | GCACCANTNA | 600 |
| CTGTNNANCT | TTAGNCCNTG | GTCCTCNTGG | GTTGNNCTTG | AACCTAATCN | CCNNTCAACT | 660 |
| GGGACAAGGT | AANTNGCCNT | CCTTTNAATT | CCCNANCNTN | CCCCCTGGTT | TGGGGTTTNT | 720 |
| CNCNCTCCTA | CCCCAGAAAN | NCCGTGTTCC | CCCCCAACTA | GGGGCCNAAA | CCNNTTNTTC | 780 |
| CACAACCCCTN | CCCCACCCAC | GGGTTGNGNT | GTTTNG | | | 816 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| CCAAGGCCTG | GGCAGGCATA | NACTTGAAGG | TACAACCCCA | GGAACCCCTG | GTGCTGAAGG | 60 |
| ATGTGGAAAA | CACAGATTGG | CGCCTACTGC | GGGGTGACAC | GGATGTCAGG | GTAGAGAGGA | 120 |
| AAGACCCAAA | CCAGGTGGAA | CTGTGGGGAC | TCAAGGAANG | CACCTACCTG | TTCAGCTGA | 180 |
| CAGTGACTAG | CTCAGACCAC | CCAGAGGACA | CGGCCAACGT | CACAGTCACT | GTGCTGTCCA | 240 |
| CCAAGCAGAC | AGAAGACTAC | TGCCTCGCAT | CCAACAANGT | GGGTCGCTGC | CGGGGCTCTT | 300 |
| TCCCACGCTG | GTA CTATGAC | CCCACGGAGC | AGATCTGCAA | GAGTTTCGTT | TATGGAGGCT | 360 |
| GCTTGGGCAA | CAAGAACAAC | TACCTTCGGG | AAGAAGAGTG | CATTCTANCC | TGTCNNGGTG | 420 |
| TGCAAGGTGG | GCCTTTGANA | NGCANCTCTG | GGGCTCANGC | GACTTTCCCC | CAGGGCCCCCT | 480 |
| CCATGGAAAG | GCGCCATCCA | NTGTTCTCTG | GCACCTGTCA | GCCCACCCAG | TTCGCTGCA | 540 |
| NCAATGGCTG | CTGCATCNAC | ANTTTCCTNG | AATTGTGACA | ACACCCCCCA | NTGCCCCCAA | 600 |
| CCCTCCCAAC | AAAGCTTCCC | TGTTNAAAAA | TACNCCANTT | GGCTTTTNAC | AAACNCCCGG | 660 |
| CNCCTCCNTT | TTCCCCNNTN | AACAAAGGGC | NCTNGCNTTT | GAAGTGCCCN | AACCCNGGAA | 720 |
| TCTNCCNNGG | AAAAANTNCC | CCCCCTGGTT | CCTNNAANCC | CCTCCNCNAA | ANCTNCCCCC | 780 |
| CCC | | | | | | 783 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|-----|
| GCCCCAATTC | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCTC | TACTTTTGG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT | GTCATTGCAA | CAGAATGGGG | GAAAGGCACT | GTTCTCTTTG | 180 |
| AAGTAGGGTG | AGTCTCTAAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGTGT | TCCACACTTG | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GAAGTGCTCA | GCCATTGTGG | TGTACACCAA | GGCGACCACA | 360 |
| GCAGCTGCAA | CCTCAGCAAT | GAAGATGAGG | AGGAGGATGA | AGAAGAACGT | CNCGAGGGCA | 420 |
| CACCTTGCTCT | CCGTCTTAGC | ACCATAGCAG | CCCANGAAAC | CAAGAGCAAA | GACCACAACG | 480 |
| CCNGCTGCGA | ATGAAAGAAA | NTACCCACGT | TGACAAACTG | CATGGCCACT | GGACGACAGT | 540 |
| TGGCCCGAAN | ATCTTCAGAA | AAGGGATGCC | CCATCGATTG | AACCCCANAA | TGCCCCACTGC | 600 |
| CNACAGGGCT | GCNCCNCNCN | GAAAGAATGA | GCCATTGAAG | AAGGATCNTC | NTGGTCTTAA | 660 |
| TGAACTGAAA | CCNTGCATGG | TGGCCCCCTGT | TCAGGGCTCT | TGGCAGTGAA | TTCTGANAAA | 720 |
| AAGGAACNGC | NTNAGCCCCC | CCAAANGANA | AAACACCCCC | GGGTGTTGCC | CTGAATTGGC | 780 |
| GGCCAAGGAN | CCCTGCCCCN | G | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGAGAGCCA | GGCGTCCCTC | TGCCTGCCCA | CTCAGTGGCA | ACACCCGGGA | GCTGTTTTGT | 60 |
| CCTTTGTGGA | GCCTCAGCAG | TTCCCTCTTT | CAGAACTCAC | TGCCAAGAGC | CCTGAACAGG | 120 |
| AGCCACCATG | CAGTGCTTCA | GCTTCATTAA | GACCATGATG | ATCCTCTTCA | ATTTGCTCAT | 180 |
| CTTTCTGTGT | GGTGCAGCCC | TGTTGGCAGT | GGGCATCTGG | GTGTCAATCG | ATGGGGCATC | 240 |
| CTTTCTGAAG | ATCTTCGGGC | CACTGTCTGC | CAGTGCCATG | CAGTTTGTCA | ACGTGGGCTA | 300 |
| CTTCCTCATC | GCAGCCGGCG | TTGTGGTCTT | TGCTCTTGGT | TTCTGGGGCT | GCTATGGTGC | 360 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TAAGACGGAG | AGCAAGTGTG | CCCTCGTGAC | GTTCTTCTTC | ATCCTCCTCC | TCATCTTCAT | 420 |
| TGCTGAAGTT | GCAGCTGCTG | TGGTCGCCTT | GGTGACACC | ACAATGGCTG | AACCATTCCT | 480 |
| GACGTTGCTG | GTANTGCCTG | CCATCAANAA | AGATTATGGG | TTCCCAGGAA | AAATTCACCTC | 540 |
| AANTNTGGAA | CACCNCCATG | AAAAGGGCTC | CAATTTCTGN | TGGCTTCCCC | AACTATACCG | 600 |
| GAATTTTGAA | AGANTCNCCC | TACTTCCAAA | AAAAAANANT | TGCCTTTNCC | CCNNTTCTGT | 660 |
| TGCAATGAAA | ACNTCCCAAN | ACNGCCAATN | AAAACCTGCC | CNNNCAAAAA | GGNTCNCAAA | 720 |
| CAAAAAAANT | NNAAGGGTTN | | | | | 740 |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CCGCTGGTTG | CGCTGGTCCA | GNGNAGCCAC | GAAGCACGTC | AGCATACACA | GCCTCAATCA | 60 |
| CAAGGTCTTC | CAGCTGCCGC | ACATTACGCA | GGGCAAGAGC | CTCCAGCAAC | ACTGCATATG | 120 |
| GGATACACTT | TACTTTAGCA | GCCAGGGTGA | CAACTGAGAG | GTGTCGAAGC | TTATTCTTCT | 180 |
| GAGCCTCTGT | TAGTGGAGGA | AGATTCCGGG | CTTCAGCTAA | GTAAGTCAGC | TATGTCCCAT | 240 |
| AAGCAAACAC | TGTGAGCAGC | CGGAAGGTAG | AGGCAAAGTC | ACTCTCAGCC | AGCTCTCTAA | 300 |
| CATTGGGCAT | GTCAGCAGT | TCTCCAAACA | CGTAGACACC | AGNGGCCTCC | AGCACCTGAT | 360 |
| GGATGAGTGT | GGCCAGCGCT | GCCCCCTTGG | CCGACTTGGC | TAGGAGCAGA | AATTGCTCCT | 420 |
| GGTTCCTGCC | TGTCACCTTC | ACTTCCGCAC | TCATCACTGC | ACTGAGTGTG | GGGGACTTGG | 480 |
| GCTCAGGATG | TCCAGAGACG | TGGTTCGGCC | CCCTCNCTTA | ATGACACCGN | CCANNCAACC | 540 |
| GTCGGCTCCC | GCCGANTGNG | TTCGTCTGTC | CTGGGTCAGG | GTCTGCTGGC | CNCTACTTGC | 600 |
| AANCTTCGTC | NGGCCCCATG | AATTCACCNC | ACCGGAACCTN | GTANGATCCA | CTNNTTCTAT | 660 |
| AACCGGNCGC | CACCGCNNTT | GGAATCCAC | TCTTNTNCC | TTTACTTGAG | GGTTAAGGTC | 720 |
| ACCTTNNCG | TTACCTTGGT | CCAAACNTN | CCNTGTGTCG | ANATNGTNAA | TCNGGNCNA | 780 |
| TNCCANCCNC | ATANGAAGCC | NG | | | | 802 |

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| CNAAGCTTCC | AGGTNACGGG | CCGCNAANCC | TGACCCNAGG | TANCANAANG | CAGNCNGCGG | 60 |
| GAGCCCACCG | TCACNGGNG | GNGTCTTTAT | NGGAGGGGGC | GGAGCCACAT | CNCTGGACNT | 120 |
| CNTGACCCCA | ACTCCCNCC | NCNCANTGCA | GTGATGAGTG | CAGAACTGAA | GGTNACGTGG | 180 |
| CAGGAACCAA | GANCAAAANNC | TGCTCCNNTC | CAAGTCGGCN | NAGGGGGCGG | GGCTGGCCAC | 240 |
| GCNCATCCNT | CNAGTGCTGN | AAAGCCCCNN | CCTGTCTACT | TGTTTGGAGA | ACNGCANNNGA | 300 |
| CATGCCCAGN | GTTANATAAC | NGGCNAGAG | TNANTTTGCC | TCTCCCTTCC | GGCTGCGCAN | 360 |
| CGNGTNTGCT | TAGNGGACAT | AACCTGACTA | CTTAAGTGAA | CCCNNGAATC | TNCCNCCCCT | 420 |
| CCACTAAGCT | CAGAACAAAA | AACCTCGACA | CCACTCANIT | GTCACCTGNC | TGCTCAAGTA | 480 |
| AAGTGTACCC | CATNCCCAAT | GTNTGCTNGA | NGCTCTGNCC | TGCNTTANGT | TCGGTCCTGG | 540 |
| GAAGACCTAT | CAATTNAAGC | TATGTTTCTG | ACTGCCTCTT | GCTCCCTGNA | ACAANCNACC | 600 |
| CNNCNTTCCA | AGGGGGGGNC | GGCCCCCAAT | CCCCCAACC | NTNAATTNAN | TTTANCCCCN | 660 |
| CCCCCNGGCC | CGGCCTTTTA | CNANCNTCNN | NNACNGGGNA | AAACCNNNGC | TTTNCCEAAC | 720 |
| NNAATCCNCC | T | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC      60
CAACCCCCCTC NTCCAAATNN CCNTTTCGG GNGGGGGTTC CAAACCCAAN TTANNTTTGG      120
ANNTTAAATT AAATNTTNNT TGGNGGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA      180
TNANCTTNA TNCCTGAAA CCNGTNGNTT CAAAAAATNT TTAACCCTTA ANTCCCTCCG      240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTGTTT GAAGGNTNAA TNAANAACCC      300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTTC NTAANAANA      360
GGNNANCCCC GGTANTNAA TCCCCCNCC CCAATTATA CCGANTTTT TTNGAATTGG      420
GANCCCNCCG GAATTAACGG GGNNTTCCC TTTTGGGGGG CNGGNNCCCC CCCNTCGGG      480
GGTTNGGGNC AGGNCNNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC      540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG      600
GGGGCCTGGG ATTTNTTTC CCCTTNTNCC TCCCCCCCC CCNGGGANAG AGGTTNGNGT      660
TTTGNTCNCN GGCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCCG      720
AGTCCNTTGN AGGNTAAAN GGCCCTTNN CGGG      754

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

ATCANCCCAT GACCCCNAA NNGGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA      60
NNGTNAGNNC ACTNCNNTTN NATCACNCCC CNCCNACTAC GCCCNANANC CNACGCNCTA      120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN      180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCTC CNAAGTATTN      240
NNCNANANAT GATTTTCCTN ANCCGATTAC CCNTNCCCC TANCCCTCC CCCCCAACNA      300
CGAAGGCNCT GGNCNNAAG NNGCGNCNCC CCGCTAGNTC CCCNNCAAGT CNCNCNCTA      360
AACTCANCCN NATTACNCGC TTCNTGAGTA TCACTCCCG AATCTCACCC TACTCAACTC      420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT      480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATTT CCNAANGGCT      540
CTTTCNGACA GCATNTTTTG GTTCCCNNTT GGGTCTTAN NGAATTGCC TTCNTNGAAC      600
GGGCTCNTCT TTTCTTCGG TTANCTGGN TTCNNCCGGC CAGTTATTAT TTCCNTTTT      660
AAATTCNTNC CNTTTANTTT TGGCNTCNA AACCCCGGC CTTGAAAACG GCCCCCTGGT      720
AAAAGTTGT TTTGANAANA TTTTGTGTTT GTTCC      755

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTANGTG | TNGTCGTGCA | GGTAGAGGCT | TACTACAANT | GTGAANACGT | 60 |
| ACGCTINGGAN | TAANGCGACC | CGANTTCTAG | GANNCNCCCT | AAAATCANAC | TGTGAAGATN | 120 |
| ATCCTGNNNA | CGGAANGGTC | ACCGGNNGAT | NNTGCTAGGG | TGNCCNCTCC | CANNNCNTTN | 180 |
| CATAACTCNG | NGGCCCTGCC | CACCACCTTC | GGCGGCCCN | NGNCCGGGCC | CGGGTCATTN | 240 |
| GNNTTAACCN | CACTNNGCNA | NCGGTTTCCN | NCCCCNNCNG | ACCCNGGCGA | TCCGGGGTNC | 300 |
| TCTGTCTTCC | CCTGNAGNCN | ANAAANTGGG | CCNCGGNCCC | CTTTACCCCT | NNACAAGCCA | 360 |
| CNGCCNTCTA | NCCNCNGCCC | CCCCTCCANT | NNGGGGGA | GCCNANNGCT | CCGTTNCTNG | 420 |
| NNACCCCNMN | GGGTNCCTCG | GTTGTGANT | CNACCGNANG | CCANGGATT | CNAAGGAAGG | 480 |
| TGCGTTNTTG | GCCCCTACCC | TTCGCTNCGG | NNACCCCTTC | CCGACNANGA | NCCGCTCCCG | 540 |
| CNCNCGNNG | CCTCNCCTCG | CAACACCCGC | NCTCNCNCT | NCGGNNNCCC | CCCCACCCGC | 600 |
| NCCCTCNCN | NGNCGNANCN | CTCCNCCNCC | GTCTCANNCA | CCACCCCGCC | CCGCCAGGCC | 660 |
| NTCANCCACN | GGNNGACNNG | NAGCNCNNTC | GCNCCGCGCN | GCGNCCCT | CGCCNCNGAA | 720 |
| CTNCNCTNCG | CCANTNCGC | TCAANCCNNA | CNAAACGCCG | CTGCGCGGCC | CGNAGCGNCC | 780 |
| NCCTCCNCGA | GTCCTCCCGN | CTTCCNACCC | ANGNNTTCN | CGAGGACACN | NNACCCCGCC | 840 |
| NNCANGCGG | | | | | | 849 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GCGCAAACTA | TACTTCGCTC | GNACTCGTGC | GCCTCGCTNC | TCTTTTCCTC | CGCAACCATG | 60 |
| TCTGACNANC | CCGATTNGGC | NGATATCNAN | AAGNTCGANC | AGTCCAAACT | GANTAACACA | 120 |
| CACACNANAN | AGANAAATCC | NCTGCCTTCC | ANAGTANACN | ATTGAACNNG | AGAACCANGC | 180 |
| NGGCGAATCG | TAATNAGGCG | TGCGCCGCCA | ATNTGTCNCC | GTTTATTNTN | CCAGCNTCNC | 240 |
| CTNCCNACCC | TACNTCTTCN | NAGCTGTCCN | ACCCCTNGTN | CGNACCCCCC | NAGGTCCGGA | 300 |
| TGCGGTTTNN | NNTGACCGNG | CNNCCCTCC | CCCNTCCAT | NACGANCCNC | CCGCACCACC | 360 |
| NANNGCNCGC | NCCCCGNCT | CTTCGCCNCC | CTGTCTTNTN | CCCCTGTNGC | CTGGCNCNGN | 420 |
| ACCGCATTGA | CCCTCGCCNN | CTNCNNGAAA | NCGNANACGT | CCGGGTTGNN | ANNANCGCTG | 480 |
| TGGGNNNGCG | TCTGCNCCGC | GTTCTTCCN | NCNCTTCCA | CCATCTTCNT | TACNNGGTCT | 540 |
| CCNCGCCNTC | TCNNNCACNC | CCTGGGACGC | TNTCTNTG | CCCCCTTAC | TCCCCCCTT | 600 |
| CGNCGTGNCC | CGNCCCCACC | NTCATTNCA | NACGNTCTTC | ACAANNCT | GGNTNNCTCC | 660 |
| CNANCNGNCN | GTCAACCCNAG | GGAAGGGNGG | GGNCCNNTG | NTTGACGTTG | NGGNGANGTC | 720 |
| CGAANANTCC | TCNCCNTCAN | CNCTACCCCT | CGGGCGNCT | CTCNGTTNCC | AACCTANCAA | 780 |
| NTCTCCCCCG | NGNGCNCNTC | TCAGCCTCNC | CCNCCCNCT | CTCTGCANTG | TNCTCTGCTC | 840 |
| TNACCNNTAC | GANTNTTCGN | CNCCCTCTTT | CC | | | 872 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GCATGCAAGC | TTGAGTATTC | TATAGNGTCA | CCTAAATANC | TTGGCNTAAT | CATGGTCNTA | 60 |
| NCTGNCTTCC | TGTGTCAAAT | GTATACNAAN | TANATATGAA | TCTNATNTGA | CAAGANNNGTA | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCNTNCATTA | GTAACAANTG | TNNTGTCCAT | CCTGTCNGAN | CANATTCCCA | TNNATTNCGN | 180 |
| CGCATTNCN | GCNCANTATN | TAATNGGGAA | NTCNNNTNN | NCACCNNCAT | CTATCNTNCC | 240 |
| GCNCCCTGAC | TGGNAGAGAT | GGATNANTTC | TNNTNTGACC | NACATGTTCA | TCTTGGATTN | 300 |
| AANANCCCC | CGCNGNCCAC | CGGTTNGNNG | CNAGCCNNTC | CCAAGACCTC | CTGTGGAGGT | 360 |
| AACCTGCGTC | AGANNCATCA | AACNTGGGAA | ACCCGCNNCC | ANGTNNAAGT | NGNNNCANAN | 420 |
| GATCCCGTCC | AGGNTTNACC | ATCCCTTCNC | AGCGCCCCCT | TTNGTGCCTT | ANAGNGNAGC | 480 |
| GTGTCCNANC | CNCTCAACAT | GANACGCGCC | AGNCCANCCG | CAATTNGGCA | CAATGTCGNC | 540 |
| GAACCCCTTA | GGGGGANTNA | TNCAANCC | CAGGATTGTC | CNCNCANGAA | ATCCNCANC | 600 |
| CCNCCCTAC | CCNCTTTGG | GACNGTGACC | AANTCCCGGA | GTNCCAGTCC | GGCCNGNCTC | 660 |
| CCCCACCGGT | NNCCNTGGGG | GGGTGAANCT | CNGNNTCANC | CNGNCGAGGN | NTCGNAAGGA | 720 |
| ACCGGNCCTN | GGNCGAANNG | ANCNNTCNGA | AGNGCCNCNT | CGTATAACCC | CCCCTCNCCA | 780 |
| NCCNACNGNT | AGNTCCCCC | CNGGGTNCGG | AANGG | | | 815 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGAGATGTC | TCGCTCCGTG | GCCTTAGCTG | TGCTCGCGCT | ACTCTCTCTT | TCTGGCCTGG | 60 |
| AGGCTATCCA | GCGTACTCCA | AAGATTCAAG | TTTACTCACG | TCATCCAGCA | GAGAATGGAA | 120 |
| AGTCAAATTT | CCTGAATTGC | TATGTGTCTG | GGTTTCATCC | ATCCGACATT | GAANTTGACT | 180 |
| TACTGAAGAA | TGGANAGAGA | ATTGAAAAAG | TGGAGCATTC | AGACTTGTCT | TTCAGCAAGG | 240 |
| ACTGGTCTTT | CTATCTCNTG | TACTACACTG | AATTCACCCC | CACTGAAAAA | GATGAGTATG | 300 |
| CCTGCCGTGT | GAACCATGTG | ACTTTGTCTC | AGCCCAAGAT | AGTTAAGTGG | GATCGAGACA | 360 |
| TGTAAGCAGN | CNNCATGGAA | GTTTGAAGAT | GCCGCATTTG | GATTGGATGA | ATTCCAAATT | 420 |
| CTGCTTGCTT | GCNTTTTAAT | ANTGATATGC | NTATACACCC | TACCCCTTAT | GNCCCCAAAT | 480 |
| TGTAGGGGTT | ACATNANTGT | TCNCNTNGGA | CATGATCTTC | CTTTATAANT | CCNCCNTTCG | 540 |
| AATTGCCCGT | CNCCNGTTN | NGAATGTTTC | CNNAACCACG | GTTGGCTCCC | CCAGGTCNCC | 600 |
| TCTTACGGAA | GGGCGTGGG | CNCTTTNCAA | GGTTGGGGGA | ACCNAAAATT | TCNCTTNTGC | 660 |
| CCNCCNCCA | CNNTCTTGNG | NNCNCANTTT | GGAACCCTTC | CNATTCCTTC | TGGCCTCNNA | 720 |
| NCCTTNNCTA | ANAAAATTN | AAANCGTNGC | NAAANNTTTN | ACTTCCCCC | TTACC | 775 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ANATTANTAC | AGTGAATCT | TTTCCCAGAG | GTGTGTANAG | GGAACGGGGC | CTAGAGGCAT | 60 |
| CCCANAGATA | NCTTATANCA | ACAGTGCTTT | GACCAAGAGC | TGCTGGGCAC | ATTTCTGCA | 120 |
| GAAAAGGTGG | CGGTCCCCAT | CACTCCTCCT | CTCCCATAGC | CATCCAGAG | GGGTGAGTAG | 180 |
| CCATCANGCC | TTCCGTGGGA | GGGAGTCANG | GAAACAACAN | ACCACAGAGC | ANACAGACCA | 240 |
| NTGATGACCA | TGGGCGGGAG | CGAGCCTCTT | CCCTGNACCG | GGGTGGCANA | NGANAGCCTA | 300 |
| NCTGAGGGGT | CACACTATAA | ACGTTAACGA | CCNAGATNAN | CACCTGCTTC | AAGTGCACCC | 360 |
| TTCTTACCTG | ACNACCAGNG | ACCNNNAACT | GCNGCCTGGG | GACAGCNCTG | GGANCAGCTA | 420 |
| ACNNAGCACT | CACCTGCCCC | CCCATGGCCG | TNCGCNTCCC | TGGTCTTGNC | AAGGGAAGCT | 480 |
| CCCTGTTGGA | ATTNCGGGGA | NACCAAGGGA | NCCCCCTCCT | CCANCTGTGA | AGGAAAAANN | 540 |
| GATGGAATTT | TNCCCTCCG | GCCNNTCCCC | TCTTCTTTA | CACGCCCCCT | NNTACTCNTC | 600 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCCCTCTNTT | NTCCTGNCNC | ACTTTTNACC | CCNNNATTTT | CCTTNATTGA | TCGGANNCTN | 660 |
| GANATTCCAC | TNNCGCCTNC | CNTCNATCNG | NAANACNAAA | NACTNTCTNA | CCNNGGGGAT | 720 |
| GGGNNCCTCG | NTCATCCTCT | CTTTTTCNCT | ACCNCNNNTT | CTTTGCCTCT | CCTTNGATCA | 780 |
| TCCAACCNTC | GNTGGCCNTN | CCCCCCNNN | TCCTTTNCCC | | | 820 |

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| TCTGGGTGAT | GGCCTCTTCC | TCCTCAGGGA | CCTCTGACTG | CTCTGGGCCA | AAGAATCTCT | 60 |
| TGTTTCTTCT | CCGAGCCCCA | GGCAGCGGTG | ATTCAGCCCT | GCCCAACCTG | ATTCTGATGA | 120 |
| CTGCGGATGC | TGTGACGGAC | CCAAGGGGCA | AATAGGGTCC | CAGGGTCCAG | GGAGGGGCGC | 180 |
| CTGCTGAGCA | CTTCCGCCCC | TCACCTGCC | CAGCCCCCTGC | CATGAGCTCT | GGGCTGGGTC | 240 |
| TCCGCCTCCA | GGTTTCTGCT | CTTCCANGCA | NGCCANCAAG | TGGCGCTGGG | CCACACTGGC | 300 |
| TTCTTCCTGC | CCNTCCCTG | GCTCTGANTC | TCTGTCTTCC | TGTCCTGTGC | ANGCNCCTTG | 360 |
| GATCTCAGTT | TCCCTCNCTC | ANNGAACTCT | GTTTCTGANN | TCTTCANTTA | ACTNTGANTT | 420 |
| TATNACCNAN | TGGNCTGTNC | TGTCNNACTT | TAATGGGCCN | GACCGGCTAA | TCCCTCCCTC | 480 |
| NCTCCCTTCC | ANTTCNNNNA | ACCNGCTTNC | CNTCNTCTCC | CCNTANCCCG | CCNGGGAANC | 540 |
| CTCCTTTGCC | CTNACCANGG | GCCNNNACCG | CCCNTNNCTN | GGGGGGCNGG | GTNNCTNCNC | 600 |
| CTGNTNNCCC | CNCTCNCNNT | TNCCTCGTCC | CNNCNCNCGN | NNGCANNTTC | NCNGTCCCN | 660 |
| TNNCTCTTCN | NGTNTCGNAA | NGNTCNCNTN | TNNNNNGNCN | NGNTNNNTCN | TCCCTCTCNC | 720 |
| CNNNTGNANG | TNNTTNNNNC | NCNGNNCCCC | NNNNCNNNNN | NGGNNNTNNN | TCTNCNCNGC | 780 |
| CCCNNCCCCC | NGNATTAAGG | CCTCCNNTCT | CCGGCCNC | | | 818 |

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGAAGGGCG | GAGGGATATT | GTANGGGATT | GAGGGATAGG | AGNATAANGG | GGGAGGTGTG | 60 |
| TCCCAACATG | ANGGTGNNGT | TCTCTTTTGA | ANGAGGGTTG | NGTTTTTANN | CCNGGTGGGT | 120 |
| GATTNAACCC | CATTGTATGG | AGNNAAAGGN | TTTNAGGGAT | TTTTCGGCTC | TTATCAGTAT | 180 |
| NTANATTCCT | GTNAATCGGA | AAATNATNTT | TCNNCNGGAA | AATNTTGCTC | CCATCCGNAA | 240 |
| ATTNCTCCCG | GGTAGTGCAT | NTTNGGGGNN | CNGCCANGTT | TCCCAGGCTG | CTANAATCGT | 300 |
| ACTAAAGNTT | NAAGTGGGAN | TNCAAATGAA | AACCTNNCAC | AGAGNATCCN | TACCCGACTG | 360 |
| TNNNTTNCCT | TCGCCCTNTG | ACTCTGCNNG | AGCCCAATAC | CCNNGNGNAT | GTNCCCNNGN | 420 |
| NNNGCGNCNC | TGAAANNNNC | TCGNGGCTNN | GANCATCANG | GGGTTTCGCA | TCAAAAGCNN | 480 |
| CGTTTCNCAT | NAAGGCACTT | TNGCCTCATC | CAACCNTNG | CCCTCNNCCA | TTTNGCCGTC | 540 |
| NGGTTNCNCT | ACGCTNNTNG | CNCCTNNNTN | GANATTTTNC | CCGCTNGGGG | NAANCCTCCT | 600 |
| GNAATGGGTA | GGGNTTNTC | TTTTNACCNN | NGGGTNTACT | AATCNNCTNC | ACGCTNCTT | 660 |
| TCTCNACCCC | CCCCCTTTT | CAATCCCANC | GGCNAATGGG | GTCTCCCCNN | CGANGGGGGG | 720 |
| NNNCCANN C | | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT      60
CGCTCANACC TCACANCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNNT      120
ATNTNTACNC TCATANNCTT CNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN      180
TNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNAT CTCTATCTCC      240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN      300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTTCNC ATNANCTCCT AATTGGAATC      360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCTCCCCC NACNATNTCT CAACCAAATC      420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCTCCG ATCCCCNNAC AACCCCCCTC      480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCAATTAN      540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNCNNAT CTCCTAANA      600
AATNCTCCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAACNNAA CCCCTGTTTT      660
TANATCCCTT CTTCGAAAA CCNACCCTTT ANNNCCCAAC CTTTNGGGCC CCCCNCCTNC      720
CCNAATGAAG GNCNCCCAAT CNANGAAACG NCCNTGAAAA ANCNAGGCNA ANANNNTCCG      780
CANATCCTAT CCCTTANTTN GGGGNCCTT NCCNGGGGCC CC                        822

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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

CGGCCGCCTG CTCTGGCACA TGCCTCCTGA ATGGCATCAA AAGTGATGGA CTGCCCATTG      60
CTAGAGAAGA CCTTCTCTCC TACTGTCAAT ATGGAGCCCT GCAGACTGAG GGCTCCCCTT      120
GTCTGCAGGA TTTGATGTCT GAAGTCGTGG AGTGTGGCTT GGAGCTCCTC ATCTACATNA      180
GCTGGAAGCC CTGGAGGGCC TCTCTCGCCA GCCTCCCCCT TCTCTCCAG CTCTCCANGG      240
ACACCAGGGG CTCAGGCAG CCCATTATT CCAGNANGAC ATGGTGTTTC TCCACGCGGA      300
CCCATGGGGC CTGNAAGGCC AGGGTCTCCT TTGACACCAT CTCTCCCGTC CTGCCTGGCA      360
GGCCGTGGGA TCCACTANTT CTANAACGGN CGCCACCNCG GTGGGAGCTC CAGCTTTTGT      420
TCCNNTTAAT GAAGGTTAAT TGCNCGCTTG GCGTAATCAT NGGTCANAAC TTTTCCTGT      480
GTGAAATTGT TTNTCCCCTC NCNATTCCNC NCNACATACN AACCCGGAAN CATAAAGTGT      540
TAAAGCCTGG GGGTNGCCTN NNGAATNAAC TNAACTCAAT TAATTGCGTT GGCTCATGGC      600
CCGCTTTCCN TTCNGGAAAA CTGTCNTCCC CTGCNTTNNT GAATCGGCCA CCCCCNNGG      660
AAAAGCGGTT TGCNTTTTNG GGGGNTCCTT CCNCTTCCCC CCTCNCTAAN CCCTNCGCCT      720
CGGTCGTTNC NGGTNGCGGG GAANGGNAT NNNCTCCNC NAAGGGGNG AGNNNGNTAT      780
CCCCAAA                                           787

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTGGC | GATGCTACTG | TTTAATTGCA | GGAGGTGGGG | GTGTGTGTAC | 60 |
| CATGTACCAG | GGCTATTAGA | AGCAAGAAGG | AAGGAGGGAG | GGCAGAGCGC | CCTGCTGAGC | 120 |
| AACAAAGGAC | TCCTGCAGCC | TTCTCTGTCT | GTCTCTTGGC | GCAGGCACAT | GGGGAGGCCT | 180 |
| CCCGCAGGGT | GGGGGCCACC | AGTCCAGGGG | TGGGAGCACT | ACANGGGGTG | GGAGTGGGTG | 240 |
| GTGGCTGGTN | CNAATGGCCT | GNCACANATC | CCTACGATTC | TTGACACCTG | GATTTACCA | 300 |
| GGGGACCTTC | TGTTCTCCCA | NGGNAACTTC | NTNNATCTCN | AAAGAACACA | ACTGTTTCTT | 360 |
| CNGCANTTCT | GGCTGTTTCT | GGAAAGCACA | GGTGTCCNAT | TTNGGCTGGG | ACTTGGGTACA | 420 |
| TATGGTTCCG | GCCCACCTCT | CCNTTCNAAN | AAGTAATTCA | CCCCCCCCCN | CCNTCTNTTG | 480 |
| CCTGGGCCCT | TAANTACCCA | CACCGGAAC | CANTTANTTA | TTTATCTTNG | GNTGGGCTTG | 540 |
| NTNATCCN | CCTGAANGCG | CCAAGTTGAA | AGGCCACGCC | GTNCCCNCTC | CCCATAGNAN | 600 |
| NTTTTNNCNT | CANCTAATGC | CCCCCNGGC | AACNATCCAA | TCCCCCCCCN | TGGGGGCCCC | 660 |
| AGCCCCANGGC | CCCCGNCTCG | GGNNCCNGN | CNCGNANTCC | CCAGGNTCTC | CCANTCNGNC | 720 |
| CCNNNGNCNC | CCCGCACGCA | GAACANAAGG | NTNGAGCCNC | CGCANNNNNN | NGGTNNCNC | 780 |
| CTCGCCCCCC | CCNNCGNNG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| TTTTNCCNAG | GGCAGGTTTA | TTGACAACCT | CNCGGGACAC | AANCAGGCTG | GGGACAGGAC | 120 |
| GGCAACAGGC | TCCGGCGGCG | GCGGCGGCGG | CCCTACCTGC | GGTACCAAAT | NTGCAGCCTC | 180 |
| CGCTCCCGCT | TGATNTTCCT | CTGCAGCTGC | AGGATGCCNT | AAACAGGGC | CTCGGCCNTN | 240 |
| GGTGGGCACC | CTGGGATTIN | AATTTCCACG | GGCACAATGC | GGTCGCANCC | CCTCACCACC | 300 |
| NATTAGGAAT | AGTGGTNTTA | CCNCCNCCG | TTGGCNCAC | CCCCNTGGAA | ACCACTTNTC | 360 |
| GCGGCTCCGG | CATCTGGTCT | TAAACCTTGC | AAACNCTGGG | GCCCTCTTTT | TGGTTANTNT | 420 |
| NCCNGCCACA | ATCATNACTC | AGACTGGCNC | GGGCTGGCCC | CAAAAAANCN | CCCCAAAACC | 480 |
| GGNCCATGTC | TTNNCGGGGT | TGCTGCNATN | TNCATCACCT | CCCGGGCNCA | NCAGGNCAAC | 540 |
| CCAAAAGTTC | TTNGGGCCCN | CAAAAAANCT | CCGGGGGGNC | CCAGTTTCAA | CAAAGTCATC | 600 |
| CCCCTTGGCC | CCCAAATCCT | CCCCCGNTT | NCTGGGTTTG | GGAACCCACG | CCTCTNNCTT | 660 |
| TGGNNGGCAA | GNTGGNTCCC | CCTTCGGGCC | CCCGTGGGC | CCNCTCTAA | NGAAAACNCC | 720 |
| NTCCTNNNCA | CCATCCCCC | NNGNACGNC | TANCAANGNA | TCCCTTTTTT | TANAAACGGG | 780 |
| CCCCCNCG | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GACAGAACAT | GTTGGATGGT | GGAGCACCTT | TCTATACGAC | TTACAGGACA | GCAGATGGGG | 60 |
| AATTCATGGC | TGTTGGAGCA | ATANAACCCC | AGTTCTACGA | GCTGCTGATC | AAAGGACTTG | 120 |
| GACTAAAGTC | TGATGAACCT | CCCAATCAGA | TGAGCATGGA | TGATTGGCCA | GAAATGAANA | 180 |
| AGAAGTTTGC | AGATGTATTT | GCAAAGAAGA | CGAAGGCAGA | GTGGTGTCAA | ATCTTTGACG | 240 |
| GCACAGATGC | CTGTGTGACT | CCGGTTCTGA | CTTTTGAGGA | GGTGTTCAT | CATGATCACA | 300 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| ACAANGAACG | GGGCTCGTTT | ATCACCANTG | AGGAGCAGGA | CGTGAGCCCC | CGCCCTGCAC | 360 |
| CTCTGCTGTT | AAACACCCCA | GCCATCCCTT | CTTTCAAAAAG | GGATCCACTA | CTTCTAGAGC | 420 |
| GGNCGCCACC | GCGGTGGAGC | TCCAGCTTTT | GTTCCCTTTA | GTGAGGGTTA | ATTGCGCGCT | 480 |
| TGGCGTAATC | ATGGTCATAN | CTGTTTCCTG | TGTGAAATTG | TTATCCGCTC | ACAATTCCAC | 540 |
| ACAACATACG | ANCCGGAAGC | ATNAAATTTT | AAAGCCTGGN | GGTNGCCTAA | TGANTGAACT | 600 |
| NACTCACATT | AATTTGGCTT | GCGCTCACTG | CCCCGTTTCC | AGTCCGGAAG | ACCTGTCCTT | 660 |
| GCCAGCTGCC | NTTAATGAAT | CNGGCCACCC | CCCGGGGAAA | AGGCNGTTTG | CTTNTTGGGG | 720 |
| CGCNCTTCCC | GCTTCTCGC | TTCCTGAANT | CCTTCCCCCC | GGTCTTTCGG | CTTGCGGCNA | 780 |
| ACGGTATCNA | CCT | | | | | 793 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCGCGACCG | GCATGTACGA | GCAACTCAAG | GGCGAGTGGA | ACCGTAAAAG | CCCCAATCTT | 60 |
| ANCAAGTGCG | GGGAANAGCT | GGGTCGACTC | AAGCTAGTTC | TTCTGGAGCT | CAACTTCTTG | 120 |
| CCAACCCACG | GGACCAAGCT | GACCAAACAG | CAGCTAATTC | TGGCCCGTGA | CATACTGGAG | 180 |
| ATCGGGGGCC | AATGGAGCAT | CCTACGCAAN | GACATCCCCT | CCTTCGAGCG | CTACATGGCC | 240 |
| CAGCTCAAAT | GCTACTACTT | TGATTACAAN | GAGCAGCTCC | CCGAGTCAGC | CTATATGCAC | 300 |
| CAGCTCTTGG | GCCTCAACCT | CCTCTTCCTG | CTGTCCCAGA | ACCGGGTGGC | TGANTNCCAC | 360 |
| ACGGANTTGG | ANCGGCTGCC | TGCCCAANGA | CATACANACC | AATGTCTACA | TCNACCACCA | 420 |
| GTGTCTTGGA | GCAATACTGA | TGGANGGCAG | CTACCNCAAA | GTNTTCCTGG | CCNAGGGTAA | 480 |
| CATCCCCCGC | CGAGAGCTAC | ACCTTCTTCA | TTGACATCCT | GCTCGACACT | ATCAGGGATG | 540 |
| AAAATCGCNG | GGTTGCTCCA | GAAAGGCTNC | AANAANATCC | TTTTCNCTGA | AGGCCCCCGG | 600 |
| ATNCNCTAGT | NCTAGAATCG | GCCCGCCATC | GCGGTGGANC | CTCCAACCTT | TCGTTNCCCT | 660 |
| TTACTGAGGG | TTNATTGCCG | CCCTTGCGGT | TATCATGGTC | ACNCCNGTTN | CCTGTGTTGA | 720 |
| AATNTTTAAC | CCCCACAAT | TCCACGCCNA | CATTNG | | | 756 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GGGGATCTCT | ANATCNACCT | GNATGCATGG | TTGTCGGTGT | GGTCGCTGTC | GATGAANATG | 60 |
| AACAGGATCT | TGCCCTTGAA | GCTCTCGGCT | GCTGTNTTTA | AGTTGCTCAG | TCTGCCGTCA | 120 |
| TAGTCAGACA | CNCTCTTGGG | CAAAAAACAN | CAGGATNTGA | GTCTTGATTT | CACCTCCAAT | 180 |
| AATCTTCNGG | GCTGCTGCT | CGGTGAAGCT | GATGACNANG | GGCAGCTGGT | TGTGNTGAT | 240 |
| AAANTCCANC | ANGTTCCTCT | TGGTGACCTC | CCCTTCAAAG | TTGTTCCGGC | CTTCATCAAA | 300 |
| CTTCTNNAAN | ANGANNANCC | CANCTTTGTC | GAGCTGGNAT | TTGGANAACA | CGTCACTGTT | 360 |
| GGAAACTGAT | CCCAAATGGT | ATGTCATCCA | TCGCCTCTGC | TGCCTGCAAA | AAACTTGCTT | 420 |
| GGCNCAAATC | CGACTCCCCN | TCCTTGAAAG | AAGCCNATCA | CACCCCCCTC | CCTGGACTCC | 480 |
| NNCAANGACT | CTNCCGCTNC | CCCNTCCNNG | CAGGGTTGGT | GGCANNCCGG | GCCCNCTGCGC | 540 |
| TTCTTCAGCC | AGTTCACNAT | NTTCATCAGC | CCCTCTGCCA | GCTGTNTAT | TCCTTGGGGG | 600 |
| GGAANCCGTC | TCTCCCTTCC | TGAANNAACT | TTGACCGTNG | GAATAGCCGC | GCNTCNCCNT | 660 |
| ACNTNCTGGG | CCGGGTTCAA | ANTCCCTCCN | TTGNCNNTCN | CCTCGGGCCA | TTCTGGATTT | 720 |
| NCCNAACTTT | TTCTTCCCC | CNCCCNCCG | NGTTTGGNTT | TTTCATNGGG | CCCCAACTCT | 780 |

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC

834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGNCGCTTT | CCNGCCGCGC | CCCGTTTCCA | TGACNAAGGC | TCCCTTCANG | TTAAATACNN | 60 |
| CCTAGNAAAC | ATTAATGGGT | TGCTCTACTA | ATACATCATA | CNAACCAGTA | AGCCTGCCCA | 120 |
| NAACGCCAAC | TCAGGCCATT | CCTACCAAAG | GAAGAAAGGC | TGGTCTCTCC | ACCCCTGTGA | 180 |
| GGAAAGGCCT | GCCTTGTAAG | ACACCACAAT | NCGGCTGAAT | CTNAAGTCTT | GTGTTTACT | 240 |
| AATGGAAAAA | AAAAATAAAC | AANAGGTTT | GTTCTCATGG | CTGCCACCG | CAGCCTGGCA | 300 |
| CTAAACANC | CCAGCGCTCA | CTTCTGCTTG | GANAAATATT | CTTTGCTCTT | TTGGACATCA | 360 |
| GGCTTGATGG | TATCACTGCC | ACNTTTCAC | CCAGCTGGGC | NCCCTTCCCC | CATNTTTGTC | 420 |
| ANTGANCTGG | AAGGCCTGAA | NCTTAGTCTC | CAAAAGTCTC | NGCCCACAAG | ACCGGCCACC | 480 |
| AGGGGANGTC | NTTNCAGTG | GATCTGCCAA | ANANTACCCN | TATCATCNNT | GAATAAAAAG | 540 |
| GCCCCTGAAC | GANATGCTTC | CANCANCCTT | TAAGACCCAT | AATCCTNGAA | CCATGGTGCC | 600 |
| CTTCCGCTCT | GATCCNAAAG | GAATGTTCTT | GGGTCCCANT | CCCTCCTTTG | TTNCTTACGT | 660 |
| TGINTTGGAC | CCNTGCTNGN | ATNACCCAAN | TGANATCCCC | NGAAGCACCC | TNCCCCTGGC | 720 |
| ATTTGANTTT | CNTAAATTCT | CTGCCCTACN | NCTGAAAGCA | CNATTCCTN | GGCNCNAAN | 780 |
| GGNGAACTCA | AGAAGGTCTN | NGAAAACCA | CNCN | | | 814 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCATGCTGCT | CTTCCTCAAA | GTTGTTCTTG | TTGCCATAAC | AACCACCATA | GGTAAAGCGG | 60 |
| GCGCAGTGTT | CGCTGAAGGG | GTTGTAGTAC | CAGCGCGGGA | TGCTCTCCTT | GCAGAGTCCT | 120 |
| GTGTCTGGCA | GGTCCACGCA | ATGCCCTTTG | TAAGTGGGGA | AATGGATGCG | CTGGAGCTCG | 180 |
| TCNAANCCAC | TCGTGTATTT | TTACANGCA | GCCTCCTCCG | AAGCNTCCGG | GCAGTTGGGG | 240 |
| GTGTCTGTCAC | ACTCCACTAA | ACTGTCGATN | CANCAGCCCA | TTGCTGCAGC | GGAAGTGGGT | 300 |
| GGGCTGACAG | GTGCCAGAAC | AACTGGATN | GGCCTTTCCA | TGGAAGGGCC | TGGGGGAAAT | 360 |
| CNCCTNANCC | CAAACTGCCT | CTCAAAGGCC | ACCTTGACCA | CCCCGACAGG | CTAGAAATGC | 420 |
| ACTCTTCTTC | CCAAAGGTAG | TTGTTCTTGT | TGCCCAAGCA | NCCTCCANCA | AACCAAANNC | 480 |
| TTGCAAAATC | TGCTCCGTGG | GGGTCATNNN | TACCANGGTT | GGGGAAANAA | ACCCGGCNGN | 540 |
| GANCCNCCTT | GTGGAATGC | NAAGGNAATA | ATCCTCCTGT | CTTGCTTGGG | TGGAANAGCA | 600 |
| CAATTGAACT | GTAAACNTTG | GGCCGNGTTC | CNCTNGGGTG | GTCTGAAACT | AATCACCGTC | 660 |
| ACTGGAAAAA | GGTANGTGCC | TTCTTGAAT | TCCCAAANTT | CCCCTNGNTT | TGGGTNNTTT | 720 |
| CTCCTCTNCC | CTAAAAATCG | TNTTCCCCCC | CCNTANGGCG | | | 760 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTAAAAA | CCCCCTCCAT | TGAATGAAAA | 60 |
| CTTCNAAAT | TGTCCAACCC | CCTCINNCAA | ATNNCCATTT | CCGGGGGGGG | GTTCCAAACC | 120 |
| CAAAATTAAT | TTGGANTTTA | AATTAAATNT | TNATTNGGGG | AANAANCCAA | ATGTNAAGAA | 180 |
| AATTTAACCC | ATTATNAACT | TAAATNCCTN | GAAACCCNTG | GNTTCCAAAA | ATTTTAAACC | 240 |
| CTTAAATCCC | TCCGAAATTG | NTAANGGAAA | ACCAAATTCN | CCTAAGGCTN | TTTGAAGGTT | 300 |
| NGATTTAAAC | CCCCTTNANT | TNTTTNACC | CNNGNCTNAA | NTATTNGNT | TCCGGTGTTT | 360 |
| TCCTNTTAAN | CNTNGGTAAC | TCCCNTAAT | GAANNCCCT | AANCCAATTA | AACCGAATTT | 420 |
| TTTTTGAAAT | GGAAATTCN | NGGGAATTNA | CCGGGGTTTT | TCCCNTTGG | GGGCCATNCC | 480 |
| CCCCTTTTCG | GGGTTGGGN | NTAGGTTGAA | TTTTNNANG | NCCCCAAAAA | NCCCCAANA | 540 |
| AAAAACTCC | CAAGNNTTAA | TTNGAATNTC | CCCCTTCCCA | GGCCTTTTGG | GAAAGGNGGG | 600 |
| TTTNTGGGGG | CCNNGGANTT | CNTTCCCCCN | TNCCNCCCC | CCCCCNGGT | AAANGGTTAT | 660 |
| NGNNTTTGGT | TTTGGGGCCC | CTTNANGGAC | CTTCCGGATN | GAAATTAAAT | CCCCGGGNGC | 720 |
| GCCG | | | | | | 724 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| TTTTTTTTTT | TTTTCTTTG | CTCACATTTA | ATTTTTATTT | TGATTTTTTT | TAATGCTGCA | 60 |
| CAACACAATA | TTTATTTTCAT | TTGTTTCTTT | TATTTTCATTT | TATTTGTTTG | CTGCTGCTGT | 120 |
| TTTATTTATT | TTTACTGAAA | GTGAGAGGGA | ACTTTTGTGG | CCTTTTTTCC | TTTTCTGTA | 180 |
| GGCCGCCTTA | AGCTTTCTAA | ATTTGGAACA | TCTAAGCAAG | CTGAANGGAA | AAGGGGGTTT | 240 |
| CGCAAAATCA | CTCGGGGGAA | NGGAAAGGTT | GCTTTGTAA | TCATGCCCTA | TGGTGGGTGA | 300 |
| TTAACTGCTT | GTACAATTAC | NTTTCACTTT | TAATTAATTG | TGCTNAANGC | TTTAATTANA | 360 |
| CTTGGGGGTT | CCCTCCCCAN | ACCAACCCCN | CTGACAAAAA | GTGCCNGCCC | TCAAATNATG | 420 |
| TCCCGGCNNT | CNTTGAAACA | CACNGCNGAA | NGTTCTCATT | NTCCCNCCNC | CAGGTNAAAA | 480 |
| TGAAGGGTTA | CCATNTTTAA | CNCCACCTCC | ACNTGGCINN | GCCTGAATCC | TCNAAAANCN | 540 |
| CCCTCAANCN | AATTNCTNNG | CCCCGGTCNC | GCNTNNGTCC | CNCCCGGCT | CCGGGAANTN | 600 |
| CACCCCNCGA | ANNCNNTNNC | NAACNAAATT | CCGAAAATAT | TCCCNNTCNC | TCAATTCCCC | 660 |
| CNNAGACTNT | CCTCNCNCAN | CNCAATTTTC | TTTTNNTCAC | GAACNCGNNC | CNNAAAATGN | 720 |
| NNNNCNCTC | CNCTNGTCN | NAATCNCCAN | C | | | 751 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGTATTTT | CTGTAAGATC | AGGTGTTTCT | CCCTCGTAGG | TTTAGAGGAA | ACACCCTCAT | 60 |
| AGATGAAAC | CCCCCGAGA | CAGCAGCACT | GCAACTGCCA | AGCAGCCGGG | GTAGGAGGGG | 120 |
| CGCCCTATGC | ACAGCTGGGC | CCTTGAGACA | GCAGGGCTTC | GATGTCAGGC | TCGATGTCAA | 180 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGGTCTGGAA | GCGGCGGCTG | TACCTGCGTA | GGGGCACACC | GTCAGGGCCC | ACCAGGAACT | 240 |
| TCTCAAAGTT | CCAGGCAACN | TCGTTGCGAC | ACACCGGAGA | CCAGGTGATN | AGCTTGGGGT | 300 |
| CGGTCATAAN | CGCGGTGGCG | TCGTCGCTGG | GAGCTGGCAG | GGCCTCCCGC | AGGAAGGCNA | 360 |
| ATAAAAGGTG | CGCCCCCGCA | CCGTTCACT | CGCACTTCTC | NAANACCATG | ANGTTGGGCT | 420 |
| CNAACCCACC | ACCANNCCGG | ACTTCCTTGA | NGGAATTCCC | AAATCTCTTC | GNTCTTGGGC | 480 |
| TTCTNCTGAT | GCCCTANCTG | GTTGCCCNNG | ATGCCAANCA | NCCCCAANCC | CCGGGGTCCT | 540 |
| AAANCAACCN | CCTCCTCNTT | TCATCTGGGT | TNTTNTCCCC | GGACNTGGT | TCCTCTCAAG | 600 |
| GGANCCCAT | TCTCNACCAN | TACTCACCT | NCCCCCCT | GNNACCCANC | CTTCTANNGN | 660 |
| TTCCCNCCCG | NCCTCTGGCC | CNTCAAANAN | GCTTNCACNA | CCTGGGTCTG | CCTTCCCCCC | 720 |
| TNCCCTATCT | GNACCCNCN | TTGTCTCAN | TNT | | | 753 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ACTATATCCA | TCACAACAGA | CATGCTTCAT | CCCATAGACT | TCTTGACATA | GCTTCAAATG | 60 |
| AGTGAACCCA | TCCTTGATTT | ATATACATAT | ATGTTCTCAG | TATTTTGGGA | GCCTTCCAC | 120 |
| TTCTTTAAAC | CTTGTTTCATT | ATGAACACTG | AAAATAGGAA | TTTGTGAAGA | GTTAAAAAGT | 180 |
| TATAGCTTGT | TTACGTAGTA | AGTTTTTGAA | GTCTACATTC | AATCCAGACA | CTTACTTGAG | 240 |
| TGTTAAACTG | TGATTTTAA | AAAATATCAT | TTGAGAATAT | TCTTTCAGAG | GTATTTTCAT | 300 |
| TTTTACTTTT | TGATTAATTG | TGTTTTATAT | ATTAGGGTAG | T | | 341 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTACTGAA | TTTAGTTCTG | TGCTCTTCCT | TATTTAGTGT | TGTATCATAA | ATACTTTGAT | 60 |
| GTTTCAAACA | TTCTAAATAA | ATAATTTTCA | GTGGCTTCAT | A | | 101 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|--|-----|
| ACATCTTTGT TACAGTCTAA GATGTGTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC | 60 |
| TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT | 120 |
| TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA | 180 |
| CCTCTTGAGA GGTCAAGTAA GAGGACTTAA TATTTTCATAT CTACAAAATG ACCACAGGAT | 240 |
| TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC | 300 |
| TCGAA | 305 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|---|-----|
| ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTGTTTTCT | 60 |
| GATTATTTGG TGTGTGTTTT GGTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT | 120 |
| CTCTCCATCC TCGGGCATTC TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT | 180 |
| CCAGAATTTT TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC | 240 |
| TGCTGTTGTT CTTCTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA | 300 |
| AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA | 360 |
| GGATGTCGCG GATGAATTCC CATAAGTGAG TCCTCTCGG GTTGTGCTTT TTGGTGTGGC | 420 |
| ACTTGGCAGG GGGGCTCTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC | 480 |
| TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTT GCTGTCCAAC AAATCTACTG | 540 |
| TGCTACCATA GTTGGTGTC TATAAATAGT TCTNGTCTT CCAGGTGTTC ATGATGGAAG | 600 |
| GCTCAGTTTG TTCAGTCTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC | 660 |
| ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCTG | 720 |
| CCGCCCGGT GAACTCTGC AACTCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC | 780 |
| CNTGGAAGG GATACAATTG GCATCCAGCT GGTGGTGTC CAGGAGGTGA TGGAGCCACT | 840 |
| CCCACACCTG GT | 852 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|---|-----|
| ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG | 60 |
| AGTCTGACAC CATCCGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGGAACTCTT | 120 |
| GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCGAGTGC | 180 |

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|---|-----|
| ACTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA | 60 |
| ATTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA | 120 |
| AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA | 240 |
| AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT | 300 |
| CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT | 360 |
| TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC | 420 |
| TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT | 540 |
| GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT | 590 |

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|--|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCCC | 60 |
| TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGGA GTTCAAGAC | 120 |
| GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAAG GGGACAAAAG CTAATCCCAA | 240 |
| AACATCAAAG AAAGGAAGGT GGCCTCATACT CTCCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCTCCAGG CTCCTGTGTG | 360 |
| CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CTGCGTGCG | 420 |
| CCACACTCCT TGAACACACA TCCCAGGTT ATATTCCTGG ACATGGCTGA ACCTCCTATT | 480 |
| CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCCTCAC CCTCCAAACC | 540 |
| ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA | 600 |
| TTCCCCTACT CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATT ACAGCTATG GGACCTTGGG CAAGTNATCT | 720 |
| TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT | 774 |

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|---|-----|
| CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT | 60 |
| TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT | 120 |
| TGGT | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|---|-----|
| GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT | 60 |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTTT TACGGGTGAT TGCAAAAATT | 120 |
| TTAGGGCACC CATATCCCAA GCANTGT | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | |
|---|-----|
| ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC | 60 |
| ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTTGGGA GAGGGGT | 107 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|---|-----|
| GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG | 60 |
| CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG | 120 |
| GCCTTGCAAG GTCAGAAAGG GGAATCAGGG CTTCACCAC AGCCCTGCCC CACTTGGCCA | 180 |
| CCTCCCTTTT GGGACCAGCA ATGT | 204 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|---|-----|
| ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA | 60 |
| GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA | 120 |
| CCATCAGACA GGTTTTAAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA | 180 |
| AAAACCTTCTT GTATCAATT CTTTGTGTTCA AAATGACTGA CTTAANTATT TTAAATATT | 240 |
| TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA | 300 |
| ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGGC | 360 |
| ATGCAACAGT GTCTTTTCTT TNCTTTTCT TTTTTTTT TTACAGGCAC AGAAACTCAT | 420 |
| CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAAATAAT CCAAGTTAAT | 480 |
| ATCACTCTTG T | 491 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|--|-----|
| ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA | 60 |
| GTATTAAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGT CTTTGATAAC | 120 |
| ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAAC ATTAGCTGCT | 180 |
| CAATCAAATC TCTACATAAC ACTATAGTAA TTAACACGTT AAAAAAAGT GTTGAAATCT | 240 |
| GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC | 300 |
| AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGT GCCTCTCCCT | 360 |
| AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCNCG | 420 |
| TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTT | 480 |
| CANT | 484 |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG      60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG      120
TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T                                151
```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCAGAAC GGACACTTTC      60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T                                91
```

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT      60
TGGATTTTGT GTATCTGTGG GTTGGGGGGA CGTCCAGGA ACCAATACCC CATGGATACC      120
AAGGGACAAC TGT                                133
```

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|---|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC | 60 |
| GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGGT | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAATAAC ATTGAATTTT CTGTATACTC | 60 |
| TGATTACATA CATTATCCT TTAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA | 120 |
| ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAGTAGTT | 180 |
| TTGACTTCTA AGTTTGGT | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|-----|
| ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT | 60 |
| CCATTGAAAA TTATCATTA TGAATTTAAA TGACAAGTTA TCAAAACTC ACTCAATTTT | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG | 240 |
| CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTTGAAGAGT | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60 |
| GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC | 120 |
| TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|-----|
| ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT | 60 |
| GGTTGTGTCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC | 120 |
| TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

| | |
|----------------------------------|----|
| CGCTCGAGCC CTATAGTGAG TCGTATTAGA | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | |
|---|----|
| ACAAGTCATT TCAGCACCTT TTGCTCTTCA AAAGTGACCA TCTTTTATAT TTAATGCTTC | 60 |
| CTGTATGAAT AAAAATGGTT ATGTCAAGT | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | |
|--|----|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTCTGCAG | 60 |
| AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT | 97 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|---|-----|
| ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACCT GGAACCCCT TTTGATGGCA | 60 |
| GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCA ACCGCACACC | 120 |
| CCAACCCTGG TCTACCCACA NTCTTGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT | 180 |
| TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA | 240 |
| GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG | 300 |
| TGGGGGTGAA CTACCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG | 360 |
| GGGCGGGAGG AGCATGT | 377 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | |
|---|-----|
| ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG | 60 |
| AGAACCCGTG TGCCCTTCC CACCATATCC ACCCTCGCTC CATCTTTGAA CTCAAACACG | 120 |
| AGGAACTAAC TGCACCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCTCCA TCCCTCACCT | 180 |
| TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT | 240 |
| TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTTT AATAAAGTCT GAAGAATTAC | 300 |
| TGTTT | 305 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|---|-----|
| ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTGTGCC CAGCACTTTA GGAATGCTGA | 60 |
| GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCAGCA GACATCAGGT CTGAGAGTTC | 120 |
| CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC | 180 |
| TGTGCTGTGC TGGAGATTCA CTTTGTAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG | 240 |
| CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG | 300 |
| CCTCTCCCAG GGGCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC | 360 |
| CATAGTTTCT GTGCTAGTGG ACCGT | 385 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|---|----|
| ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA | 60 |
| GTTTTTTTAA TGG | 73 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|--|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCCTCCT CTCCTGCAGC | 60 |
| TCCAGCTTTG TGCTCTGCCCT CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT | 120 |
| CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT | 180 |
| CCCGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT | 240 |
| CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT | 300 |
| ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG | 360 |
| CCGAACCATA TGTACCAAGT CCCAGCCCCA CTTGGACACC TGTGCCCTCC ATGAACAGCC | 420 |
| AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCTT GGGGAGAACA | 480 |
| GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | |
|---|-----|
| ATGACCCCTA ACAGGGGCCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT | 60 |
| TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA | 120 |
| CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT | 180 |
| CCAAAAAGGC CTTGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC | 240 |
| AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC | 300 |
| ACTGGCCCC AACAGGCATC ACCCCGCTAA ATCCCTAGA AGTCCCACTC CTAAACACAT | 360 |
| CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA | 420 |
| ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATT TACTGGGTCT CTATTTT | 477 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|-----|
| AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAACACA TTTTCTACAT AGATAGTACT | 60 |
| AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATTA ATAATGGTAA GATTGGTTTA | 120 |
| TGTGATTTTA GTGGTATTTT TGGCACCCTT ATATATGTTT TCCAACTTT CAGCAGTGAT | 180 |
| ATTATTTCCA TAACTAAAA AGTGAGTTTG AAAAAGAAAA TCTCCAGCAA GCATCTCATT | 240 |
| TAAATAAAGG TTTGTCATCT TAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC | 300 |
| AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA | 360 |
| AGTCAGTTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG | 420 |
| CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTTTG TATTTTAAAA AAGTACATGG | 480 |

TAAAAAAAAA AATTCACAAC AGTATATAAG GCTGTAAAT GAAGAATTCT GCC

533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | |
|---|-----|
| TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA | 60 |
| AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA | 120 |
| AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA | 180 |
| AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT | 240 |
| GAGGTTCTCT GTGTGCCCAC TGGTTTGAAC ACCGTTCTNC AATAATGATA GAATAGTACA | 300 |
| CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAAAC | 360 |
| GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCCC GTCTGTTATG | 420 |
| ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTCTAAGCA AACNCAGGTG ATGATGGCNA | 480 |
| AAATACACCC CCTCTTGAAG NACNCGGAGG A | 511 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | |
|---|-----|
| CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC | 60 |
| CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTG GGTCTTCGC | 120 |
| TGGCCTTGGT GGAGCTGGTG CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA | 180 |
| CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC | 240 |
| CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA | 300 |
| CTCTGCATTA AATCTATTTG CCATTCTGA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCG | 360 |
| ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGGCCAGC | 420 |
| CATCTGTTGT TTGCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT | 480 |
| GTCTTTTCTT AANTAAAT | 499 |

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTCAGCC GCGAAGAGAT      60
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT      120
TCCAGGCCCA CGGCTCAAGT GAATTGGAAT ACTGCATTTA CAGTGTAGAG TAACACATAA      180
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA      240
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG      300
GGCTTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC      360
CAGTTTGCTT GATATATTTG TTGATATTAA GATTCTTGAC TTATATTTTG AATGGGTTCT      420
ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTTATTTA CACTCTTGAT      480
TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT      537

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC      60
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA      120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG      180
TGGCACAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAAGCGT CTTCTGAGGA      240
TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA      300
TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA      360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC      420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN      467

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

AAGCTGACAG CATTGGGGCC GAGATGTCTC GTCCTGGTGG CTTAGCTGTG CTCGCGCTAC      60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTGAGTT TACTCAGTC      120
ATCCAGCAGA GAATGGAAAG TCAAATTTCC TGAATTGCTA TGTGTCTGGG TTTTCATCCAT      180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG      240
ACTTGCTTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA      300
CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG      360

```

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|--|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT | 60 |
| CCAGCTGCCC CGGCGGGGGA TCGAGGCTC GGAGCACCT TGCCCGGCTG TGATTGCTGC | 120 |
| CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA | 180 |
| GTTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA | 240 |
| AAAAAAA | 248 |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA | 60 |
| TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTC ATAAATGCCT | 180 |
| GATTTAAAAA AAAAAAAAAA A | 201 |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | |
|---|-----|
| TCCTTTTGTG AGGTTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG | 60 |
| TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT | 120 |
| CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG | 180 |

```

TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT      240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT      300
CTGTTTCCTTG GCTAGAAAAA ATTATAACA GGACTTTGTT AGTTTGGGAA GCCAAATTGA      360
TAATATTCTA TGTTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTTA      420
TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAAGTT TGANTNAAAC      480
CNGTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA      540
AAAAAAAAAA AA                                                              552

```

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA      60
GGGGAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TCGCTGGCA CCCCTGGCCT      120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT      180
GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA      240
AGGTTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC      300
TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC      360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGGTAC GCNTAAAAAT      420
GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTAAAAAAA AAAAAAAAAA AAAAAA      476

```

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

TTTTTTTTTG TATGCCNTCN CTGTGNGT ATTGTTGCTG CCACCCTGGA GGAGCCCACT      60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCTCCA TTCCAGCCT      120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG      180
ACTCAGTCAG CGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT              232

```

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

AGGCGGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC      60
AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG      120
GTGCCAGCCT GACCGCCACT CTCACATTG GGTCTTTCGC TGGCCTTGGT GGAGCTGGTG      180
CCAGCACCCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA CAAGTGAGAT TTTAGATATT      240
GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC      300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTG      360
CCATTTCAAA AAAAAAAAAA AAA                                     383

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA      60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC      120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA      180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG      240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAACTCT TCGGACTGTG      300
AGCCCTGATG CCTTTTGGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GCGGATTGAT      360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT      420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA      480
AAAAAAAAAA AAAA                                           494

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGA CTCTCCCA      60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCTCCAG      120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG      180
GCACACCCTC CTGGGGCCCA GCGGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG      240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAATATCC TGCTGGTCAC TTGCTCATTG      300
CCATGTTTCTG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC      360
AGCGTTNCCG CCTCATCCGG                                     380

```

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTGCCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCAC ACTTTTGATG ACTTTATTGA      240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCNT TGGTGGNNGC GCNTNCCTTT      480
T                                                                                   481
```

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGAIN TTGTCTGCTG AGAATTCATT      60
ACTTGAAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTACAC ACCTGTAAAA AGGGCGCTAA GCATTTTGA TTCAACATCT TTTTTTTGA      240
CACAAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTGTA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG                   472
```

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | |
|--|-----|
| AGAAACCAAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG | 60 |
| TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG | 120 |
| CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT | 180 |
| TTGTCTTCTG TGTAAGTGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT | 240 |
| TTTATTCGAC ATGAAGGAAA TTTCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG | 300 |
| GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA | 360 |
| ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATNAA ACGTTTTTTT TTT | 413 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | |
|---|-----|
| CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCCTCCC CGCGTCCCGC | 60 |
| GTCCTAGCCN ACCATGGCCG GGGCCCTGCG CGCCCCGCTG CTCCTGCTGG CCATCCTGGC | 120 |
| CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT | 180 |
| GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCACTG GACTTTGCCG | 240 |
| TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC | 300 |
| CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAG TTGAACCTGG GCCAAACNNG | 360 |
| TTTACCAGAA CCNAGCCAAT TNGAACAAAT NCCCCTCCAT AACAGCCCCT TTAAAAAGG | 420 |
| GAANCANTCC TGNTCTTTTC CAAATTTT | 448 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | |
|---|-----|
| GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA | 60 |
| GTAGTGATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAAATGTCA AAAAATTAGC | 120 |
| AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTTGTAG CCTTGAAGTT | 180 |
| CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CCTTGCATC | 240 |
| TTTATGTTN AGACTTGCCCT CTNTNAAAT GCTTTTGTNT TCTGCAGGTA CTATCTGTGG | 300 |
| TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTTGA ATATCTTACA TCTNAAAATN | 360 |
| AATTCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN | 420 |
| AATTCNNANA ANTTCAAGTN TCATACAACA NAACNGGANC CCC | 463 |

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | |
|---|-----|
| AGGGATTGAA GGTCTNTNT ACTGTCGGAC TGTTCANCCA CCAACTCTAC AAGTTGCTGT | 60 |
| CTTCCACTCA CTGTCTGTAA GCNTNTTAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT | 120 |
| TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTGAG TTAGTATAAG CTCTTCCACT | 180 |
| TCCTTTGTTA AGACTTCATC TGGTAAAGTC TTAAGTTTGT TAGAAAGGAA TTTAATTGCT | 240 |
| CGTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT | 300 |
| TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTGA AATTCTGCAA | 360 |
| GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA | 400 |

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | |
|--|-----|
| GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT | 60 |
| GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC | 120 |
| ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT | 180 |
| TGTGGAAAAA CTGGCACTTG NCTGGAAC TA GCAAGACATC ACTTACAAAT TCACCCACGA | 240 |
| GACACTTGAA AGGTGTAACA AAGCGACTCT TGCAATGCTT TTTGTCCCTC CGGCACCACT | 300 |
| TGTCAATACT AACCCGCTGG TTTGCCTCCA TCACATTTGT GATCTGTAGC TCTGGATACA | 360 |
| TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT | 420 |
| NGATCAGGTT CCCATTTCCT AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA | 480 |

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| ATACAGCCCA | NATCCACCA | CGAAGATGCG | CTTGTTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCGCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGGTTGATGC | TGCACTCCTT | 120 |
| CCCACGCAGG | CAGCAGCGGG | GCCGGTCAAT | GAACTCCACT | CGTGGCTTGG | GGTTGACGGT | 180 |
| TAANTGCAGG | AAGAGGCTGA | CCACCTCGCG | GTCCACCAGG | ATGCCCCGACT | GTGCGGGACC | 240 |
| TGCAGCGAAA | CTCCTCGATG | GTCATGAGCG | GGAAGCGAAT | GANGCCCAGG | GCCTTGCCCA | 300 |
| GAACCTTCCG | CCTGTTCTCT | GGCGTCACCT | GCAGCTGCTG | CCGCTNACAC | TCGGCCTCGG | 360 |
| ACCAGCGGAC | AAACGGCGTT | GAACAGCCGC | ACCTCACGGA | TGCCCANTGT | GTGCGCTCC | 420 |
| AGGAACGGCN | CCAGCGTGTC | CAGGTCAATG | TCGGTGAANC | CTCCGCGGGT | AATGGCG | 477 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | |
|------------|-------------|-------------|------------|------------|------------|-----|
| GAACGGCTGG | ACCTTGCCTC | GCATTGTGCT | GCTGGCAGGA | ATACCTTGGC | AAGCAGCTCC | 60 |
| AGTCCGAGCA | GCCCCAGACC | GCTGCCGCCC | GAAGCTAAGC | CTGCCTCTGG | CCTTCCCCTC | 120 |
| CGCCTCAATG | CAGAACCCANT | AGTGGGAGCA | CTGTGTTAG | AGTTAAGAGT | GAACACTGTN | 180 |
| TGATTTTACT | TGGGAATTTC | CTCTGTATATA | TAGCTTTTCC | CAATGCTAAT | TTCCAAACAA | 240 |
| CAACAACAAA | ATAACATGTT | TGCCTGTINA | GTTGTATAAA | AGTANGTGAT | TCTGTATNTA | 300 |
| AAGAAAATAT | TACTGTTACA | TATACTGCTT | GCAANTTCTG | TATTTATTTG | TNCTCTGGAA | 360 |
| ATAAATATAT | TATTAAA | | | | | 377 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CCCTTTGAGG | GGTTAGGGTC | CAGTTCCCAG | TGGAAGAAAC | AGGCCAGGAG | AANTGCGTGC | 60 |
| CGAGCTGANG | CAGATTTCCC | ACAGTGACCC | CAGAGCCCTG | GGCTATAGTC | TCTGACCCCT | 120 |
| CCAAGGAAAG | ACCACCTTCT | GGGGACATGG | GCTGGAGGGC | AGGACCTAGA | GGCACCAAGG | 180 |
| GAAGGCCCCA | TTCCGGGGCT | GTTCCCCGAG | GAGGAAGGGA | AGGGGCTCTG | TGTGCCCCC | 240 |
| ACGAGGAANA | GGCCCTGANT | CCTGGGATCA | NACACCCCTT | CACGTGTATC | CCCACACAAA | 300 |
| TGCAAGCTCA | CCAAGTCCC | CTCTCAGTCC | CTTCCCTACA | CCCTGAACGG | NCACTGGCCC | 360 |
| ACACCCACCC | AGANCANCCA | CCCGCCATGG | GGAATGTNCT | CAAGGAATCG | CNGGGCAACG | 420 |
| TGGACTCTNG | TCCCNNAAGG | GGGCAGAATC | TCCAATAGAN | GGANNGAACC | CTTGCTNANA | 480 |
| AAAAAAAAANA | AAAAA | | | | | 495 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
TAGCTGTTTT GAGTTGATTC GCACCACTGC ACCACAATC AATATGAAAA CTATTTNACT      180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTTGT TCATACTGTA TTTATCAAGT      240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA      300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GTAACCTCAC      360
TTGGTTATTT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA      420
TTTANTTCAN TAAATTCCTT CCTTGTTTAC GTTAATTTTG AAAAGAATGC AT              472
```

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT      60
GTGGTGAAAT TTCAAATAA TATGTAACCT CTACTAGTTT TACTTTCTCC CCCAAGTCTT      120
TTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT      180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNGCANAATG TTCTAGNTAT      240
AGCTGGATAC ATACNGTGGG AGTTCATAAA ACTCATACCT CAGTGGGACT NAACCAAAAT      300
TGGTGTTAGT TCAATTCCTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT      360
GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAAGTN ACATCTGCGT      420
TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT          476
```

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCAC AGAATGGATA      60
```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AAATAATGCT | GCAAACCTAA | TGTTCTTATG | CAAAATGGAA | CGCTAATGAA | ACACAGCTTA | 120 |
| CAATCGCAAA | TCAAAACTCA | CAAGTGCTCA | TCTGTTGTAG | ATTTAGTGTA | ATAAGACTTA | 180 |
| GATTGTGCTC | CTTCGGATAT | GATTGTTTCT | CANATCTTGG | GCAATNTTCC | TTAGTCAAAT | 240 |
| CAGGCTACTA | GAATTCTGTT | ATTGGATAIN | TGAGAGCATG | AAATTTTAA | NAATACACTT | 300 |
| GTGATTATNA | AATTAATCAC | AAATTTCACT | TATACCTGCT | ATCAGCAGCT | AGAAAAACAT | 360 |
| NTNNTTTTAA | NATCAAAGTA | TTTGTGTTT | GGAANTGTNN | AAATGAAATC | TGAATGTGGG | 420 |
| TTCNATCTTA | TTTTTTCCCN | GACNACTANT | TNCTTTTTTA | GGGNCTATTC | TGANCCATC | 479 |

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTCAG | TTTCCTCTAC | GGATGAGAGA | CTGGCTCAAG | AATATCCTCA | TGCAGCTTTA | 240 |
| TGAAGCCACT | CTGAACACGC | TGGTTATCTA | GATGAGAACA | GAGAAATAAA | GTCAGAAAAT | 300 |
| TTACCTGGAG | AAAAGAGGCT | TTGGCTGGGG | ACCATCCCAT | TGAACCTTCT | CTTAAGGACT | 360 |
| TTAAGAAAAA | CTACCACATG | TTGTGTATCC | TGGTGCCGCG | CGTTTATGAA | CTGACCACCC | 420 |
| TTTGAATAAA | TCTTGACGCT | CCTGAACCTG | CTCCTCTGCG | A | | 461 |

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGCCGCGC | GCAGGTGTTT | CCTCGTACCG | CAGGGCCCCC | TCCCTTCCCC | AGGCGTCCCT | 60 |
| CGGCGCCTCT | GCGGGCCCGA | GGAGGAGCGG | CTGGCGGGTG | GGGGGAGTGT | GACCCACCTT | 120 |
| CGGTGAGAAA | AGCCTTCTCT | AGCGATCTGA | GAGGCGTGCC | TTGGGGGTAC | C | 171 |

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGACGAA GATTCTGCCA GCAGTTGGTC    60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC    120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCAC GACCTTGACG CCGTCGGGGA    180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCTCGGG AAGGGCGGCC    240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC                                269
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA    60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCTG GTCAACTTCC TTTGTCGTGG    120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG    180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG    240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTTT AGAGAGTCCA    300
CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG    360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA                                405
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT    60
GGCACTTAAT CCATTTTTAT TTCAAAATGT CTACAAATTT AATCCCATT TACGGTATTT    120
TCAAAATCTA AATTATTCAA ATTAGCCAAA TCCTTACCAA ATAATACCCA AAAATCAAAA    180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATACGG CTGGTGTTTT    240
CAAAGTACAA TTATCTTAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT    300
CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC    360
AAATCTTAGG GGAATATATA CTTACACGG GATCTTAAC TTTACTACT TTGTTTATTT    420
TTTTAAACCA TTGTTTGGGC CCAACACAAT GGAATCCCCC CTGGACTAGT                                470
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

TTTTTTTTTT TTTTTTTTGA CCCCCTCTT ATAAAAACA AGTTACCATT TTATTTTACT      60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC      120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCCTAAAGT      180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC      240
ATTTTCTTG TCTTAAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATTT      300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTAATTATTAG TAAGTGGCTT TTTTCCTAAA      360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCAT ATTTCTACCT      420
ACGTTAATAA AATAGCATTT TGTGAAGCCA GCTCAAAGA AGGCTTAGAT CCTTTTATGT      480
CCATTTTAGT CACTAAACGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT      540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTTCT G                          581

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

TTTTTTTTTT TTTTTTTTTT TTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT      60
CACTCTCTAG ATAGGGCATG AAGAAACTC ATCTTTCCAG CTTTAAAATA ACAATCAAAT      120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA      180
AGGAAATCTG TTCAATCTTC TCATTCATAT AGTTATATCA AGTACTACCT TGCATATTGA      240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT      300
TTCATGCAAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT      360
CAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC      420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT      480
AAAGGAACAT TTTTAGCCTG GGTATAATTA GCTAATTCAC TTTACAAGCA TTTATTAGAA      540
TGAATTCACA TGTATTATT CCTAGCCCAA CACAATGG                          578

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| TTTTTTTTTT TTTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTT AAAATTCATA | 60 |
| GAAAAGTGCC TTACATTTAA TAAAAGTTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT | 120 |
| GTCCTGAACA CCAATATTAA TTTGAGGAAA ATACACCAA ATACATTAAG TAAATTATTT | 180 |
| AAGATCATAG AGCTTGTAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA | 240 |
| AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTAAATTTTG TGATGAATAT | 300 |
| GGGGTGTCAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA | 360 |
| TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTTCT CTTTCTTCAA TCTTTTAAGG | 420 |
| GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTTCTA TGGAAGGATT | 480 |
| AGATATGTTT CCTTGCCAA TATTAAAAA ATAATAATGT TTACTACTAG TGAAACCC | 538 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|---|-----|
| TTTTTTTTTT TTTTTCAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC | 60 |
| ATTTATTAGC TCTGCAACTT ACATATTTAA ATTAAAGAAA CGTTTTCAGC AACTGTACAA | 120 |
| TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCT CCAAGAGTGG ATGTGTCCCT | 180 |
| TCTCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT | 240 |
| GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG | 300 |
| AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CCGTGAAAAT | 360 |
| AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA | 420 |
| CCGCTTCCTC AAAGGCGCTG CCACATTTGT GGCTCTTTC ACTTGTTTCA AAA | 473 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|--|-----|
| CGCCATGGCA CTGCAGGGCA TCTCGGTCAT GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT | 60 |
| CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGTA CGCGTGGACC GGCCCGGCTC | 120 |
| CCGTACGAC GTGAGCCGCT TGGGCCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA | 180 |
| GCCGCGGGGA GCCGCCGTGC TCGGGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC | 240 |
| CTTCCGCCGC GGTGTCATGG AGAACTCCA GCTGGGCCCA GAGATTCTGC AGCGGAAAA | 300 |
| TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGTT | 360 |
| AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAGGTGTT CTCTCAAAA TTGGCAGAAG | 420 |
| TGGTGAGAAAT CCGTATGCCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT | 480 |
| GTGTGCACTG GGCATTATAA TGGCTCTTTT TGACCGCACA CGCACTGACA AGGGTCAGGT | 540 |

```

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTTCTGT GGAAAACCTCA    600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT    660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGGAGCAA TAGAACCCCA    720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT    780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAAGAC    840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC    900
TTTGTAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCACTGA    960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCAG CCATCCCTTC   1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACA CACTGAGGAG ATACTTGAAG AATTGGATT   1080
CAGCCGCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA   1140
AGCTAGTCTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG   1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTTA   1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA   1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACTTTGGG TACTTATACT AAATTATGGT   1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA   1440
TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT   1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT   1560
AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA   1620
A

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
          20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
          35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
          50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
          65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
          85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
          100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
          115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
          130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
          145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
          165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
          180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
          195         200         205

```

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC TGCGCCAGGG CCTGAGCGGA GGCAGGGGCA GCCTCGCCAG CGGGGGCCCC 60
 GGGCCTGGCC ATGCCTCACT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC 120
 CAGTGCAGCC TAGTGGCTCT CACCTGCTTC CTCCTGGGCG TGGGCTGCCG GCTGACCCCG 180
 GGTTCGTACC ACCTGGGCCG CACTGTCTTC TGCATCGACT TCATGGTTT CACGGTGCGG 240
 CTGCTTCACA TCTTCACGGT CAACAAACAG CTGGGGCCCA AGATCGTCAT CGTGAGCAAG 300
 ATGATGAAGG ACGTGTCTT CTTCCTCTTC TTCTCGGCG TGTGGCTGGT AGCCTATGGC 360
 GTGGCCACGG AGGGGCTCCT GAGGCCACGG GACAGTGAAT TCCCAAGTAT CCTGCGCCGC 420
 GTCTTCTACC GTCCCTACCT GCAGATCTTC GGGCAGATTC CCCAGGAGGA CATGGACGTG 480
 GCCCTCATGG AGCACAGCAA CTGCTCGTCG GAGCCCGGCT TCTGGGCACA CCCTCCTGGG 540
 GCCCAGGCGG GCACCTGCGT CTCCAGTAT GCCAACTGGC TGGTGGTGCT GCTCCTCGTC 600
 ATCTTCCTGC TCGTGGCCAA CATCCTGCTG GTCAACTTGC TCATTGCCAT GTTCAGTTAC 660
 ACATTCGGCA AAGTACAGGG CAACAGCGAT CTCTACTGGA AGGCGCAGCG TTACCGCTC 720
 ATCCGGGAAT TCCACTCTCG GCCCGCGCTG GCCCGCCCT TTATCGTCAT CTCCCACTTG 780
 CGCTCCTGCT TCAGGCAATT GTGCAGGCGA CCCCAGAGCC CCCAGCGTC CTCCCCGGCC 840
 CTCGAGCATT TCCGGGTTTA CCTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGGAA 900
 TCGGTGCATA AGGAGAACTT TCTGCTGGCA CGCGCTAGGG ACAAGCGGGA GAGCGACTCC 960
 GAGGCTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAAACAGCT GGGACACATC 1020
 CGCGAGTACG AACAGCGCCT GAAAGTGCTG GAGCGGGAGG TCCAGCAGTG TAGCCGCGTC 1080
 CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC TCTGCCTTGC TGCCCCCAGG TGGGCCGCCA 1140
 CCCCTGACC TGCTGGGTC CAAAGACTGA GCCCTGCTGG CGGACTTCAA GGAGAAGCCC 1200
 CCACAGGGGA TTTTGCTCCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG 1260
 GCCTTGTCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTGAGGACC ACCTTTGGGA 1320
 GTGTCATCCT TACAAACCAC AGCATGCCCG GCTCCTCCCA GAACCAGTCC CAGCCTGGGA 1380

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GGATCAAGGC | CTGGATCCCG | GGCCGTTATC | CATCTGGAGG | CTGCAGGGTC | CTTGGGGTAA | 1440 |
| CAGGGACCAC | AGACCCCTCA | CCACTCACAG | ATTCTCACA | CTGGGGAAT | AAAGCCATTT | 1500 |
| CAGAGGAAAA | AAAAAAAAAA | AAAA | | | | 1524 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GGGAACCAGC | CTGCACGCGC | TGGCTCCGGG | TGACAGCCGC | GCGCCTCGGC | CAGGATCTGA | 60 |
| GTGATGAGAC | GTGTCCCCAC | TGAGGTGCCC | CACAGCAGCA | GGTGTGAGC | ATGGGCTGAG | 120 |
| AAGCTGGACC | GGCACCAAAG | GGCTGGCAGA | AATGGGCGCC | TGGCTGATTC | CTAGGCAGTT | 180 |
| GGCGGCAGCA | AGGAGGAGAG | GCCGCAGCTT | CTGGAGCAGA | GCCGAGACGA | AGCAGTTCTG | 240 |
| GAGTGCCTGA | ACGGCCCCCT | GAGCCCTACC | CGCCTGGCCC | ACTATGGTCC | AGAGGCTGTG | 300 |
| GGTGAGCCGC | CTGCTGCGGC | ACCGGAAAGC | CCAGCTCTTG | CTGGTCAACC | TGCTAACCTT | 360 |
| TGGCCTGGAG | GTGTGTTTGG | CCGCAGGCAT | CACCTATGTG | CCGCCTCTGC | TGCTGGAAGT | 420 |
| GGGGGTAGAG | GAGAAGTTCA | TGACCATGGT | GCTGGGCATT | GGTCCAGTGC | TGGGCCTGGT | 480 |
| CTGTGTCCCG | CTCCTAGGCT | CAGCCAGTGA | CCACTGGCGT | GGACGCTATG | GCCGCCGCCG | 540 |
| GCCCTTCATC | TGGGCACTGT | CCTTGGGCAT | CCTGCTGAGC | CTCTTTCTCA | TCCCAAGGGC | 600 |
| CGGCTGGCTA | GCAGGGCTGC | TGTGCCCGGA | TCCCAGGCC | CTGGAGCTGG | CACTGCTCAT | 660 |
| CCTGGGCGTG | GGGCTGCTGG | ACTTCTGTGG | CCAGGTGTGC | TTCACTCCAC | TGGAGGCCCT | 720 |
| GCTCTCTGAC | CTCTTCCGGG | ACCCGGACCA | CTGTGCGCAG | GCCTACTCTG | TCTATGCCTT | 780 |
| CATGATCAGT | CTTGGGGGCT | GCCTGGGCTA | CCTCTGCCT | GCCATTGACT | GGGACACCAG | 840 |
| TGCCCTGGCC | CCCTACCTGG | GCACCCAGGA | GGAGTGCCTC | TTTGGCCTGC | TCACCCTCAT | 900 |
| CTTCCTCACC | TGCGTAGCAG | CCACACTGCT | GGTGGCTGAG | GAGGCAGCGC | TGGGCCCCAC | 960 |
| CGAGCCAGCA | GAAGGGCTGT | CGGCCCCCTC | CTTGTGCGCC | CACTGCTGTC | CATGCCGGGC | 1020 |
| CCGCTTGGCT | TTCCGGAACC | TGGGCGCCCT | GCTTCCCGG | CTGCACCAGC | TGTGCTGCCG | 1080 |
| CATGCCCCGC | ACCCTGCGCC | GGCTCTTCGT | GGCTGAGCTG | TGCAGCTGGA | TGGCACTCAT | 1140 |
| GACCTTCACG | CTGTTTACAC | CGGATTTTCG | GGGCGAGGGG | CTGTACCAGG | GCGTGCCAG | 1200 |
| AGCTGAGCCG | GGCACCAGAG | CCCGGAGACA | CTATGATGAA | GGCGTTCGGA | TGGGCAGCCT | 1260 |
| GGGCTGTGTC | CTGCACTGCG | CCATCTCCCT | GGTCTTCTCT | TGGTTCATGG | ACCGGCTGGT | 1320 |
| GCAGCGATTC | GGCACTCGAG | CAGTCTATTT | GGCCAGTGTG | GCAGCTTTCC | CTGTGGCTGC | 1380 |
| CGGTGCCACA | TGCCTGTCCC | ACAGTGTGGC | CGTGGTGACA | GCTTCAGCCG | CCCTCACCAG | 1440 |
| GITCACCTTC | TCAGCCCTGC | AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | 1500 |
| GAAGCAGGTG | TTCTTGCCCA | AATACCGAGG | GGACACTGGA | GGTGCTAGCA | GTGAGGACAG | 1560 |
| CCTGATGACC | AGCTTCCTGC | CAGGCCCTAA | GCCTGGAGCT | CCCTTCCCTA | ATGGACACGT | 1620 |
| GGGTGCTGGA | GGCAGTGGCC | TGCTCCCAAC | TCCACCCGCG | CTCTGCGGGG | CCTCTGCCTG | 1680 |
| TGATGTCTCC | GTACGTGTGG | TGGTGGGTGA | GCCCACCGAG | GCCAGGGTGG | TTCCGGGGCCG | 1740 |
| GGGCATCTGC | CTGGACCTCG | CCATCTGGA | TAGTGCTTC | CTGCTGTCCC | AGGTGGCCCC | 1800 |
| ATCCCTGTTT | ATGGGCTCCA | TTGTCCAGCT | CAGCCAGTCT | GTCAGTGCCT | ATATGGTGTC | 1860 |
| TGCCGCAGGC | CTGGGTCTGG | TCGCCATTTA | CTTTGCTACA | CAGGTAGTAT | TTGACAAGAG | 1920 |
| CGACTTTGGC | AAATACTCAG | CGTAGAAAAC | TTCCAGCACA | TTGGGGTGGG | GGGCTGCCT | 1980 |
| CACTGGGTCC | CAGCTCCCGG | CTCCTGTAG | CCCCATGGGG | CTGCCGGGCT | GGCCGCCAGT | 2040 |
| TTCTGTTGCT | GCCAAAGTAA | TGTGGCTCTC | TGCTGCCACC | CTGTGCTGCT | GAGGTGCGTA | 2100 |
| GCTGCACAGC | TGGGGGCTGG | GGCGTCCCTC | TCCTCTCTCC | CCAGTCTCTA | GGGCTGCCTG | 2160 |
| ACTGGAGGCC | TTCCAAGGGG | GTTTCAGTCT | GGACTTATAC | AGGGAGGCCA | GAAGGGCTCC | 2220 |
| ATGCACTGGA | ATGCGGGGAC | TCTGCAGGTG | GATTACCCAG | GCTCAGGGTT | AACAGCTAGC | 2280 |
| CTCCTAGTTG | AGACACACCT | AGAGAAGGGT | TTTTGGGAGC | TGAATAAACT | CAGTCACTG | 2340 |
| GTTTCCCATC | TCTAAGCCCC | TTAACCTGCA | GCTTCGTTTA | ATGTAGCTCT | TGCATGGGAG | 2400 |
| TTTCTAGGAT | GAAACACTCC | TCCATGGGAT | TGAACATAT | GACTTATTTG | TAGGGGAAGA | 2460 |
| GTCTGAGGG | GCAACACACA | AGAACCAGGT | CCCCTCAGCC | CACAGCACTG | TCTTTTGTCT | 2520 |

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| GATCCACCCC | CCTCTTACCT | TTTATCAGGA | TGTGGCCTGT | TGGTCCTTCT | GTTGCCATCA | 2580 |
| CAGAGACACA | GGCATTAAAA | TATTTAACTT | ATTTATTTAA | CAAAGTAGAA | GGGAATCCAT | 2640 |
| TGCTAGCTTT | TCTGTGTTGG | TGTCTAATAT | TTGGGTAGGG | TGGGGGATCC | CCAACAATCA | 2700 |
| GGTCCCCTGA | GATAGCTGGT | CATTGGGCTG | ATCATTGCCA | GAATCTTCTT | CTCCTGGGGT | 2760 |
| CTGGCCCCCC | AAAATGCCTA | ACCCAGGACC | TTGGAAATTC | TACTCATCCC | AAATGATAAT | 2820 |
| TCCAAATGCT | GTTACCCAAG | GTTAGGGTGT | TGAAGGAAGG | TAGAGGGTGG | GGCTTCAGGT | 2880 |
| CTCAACGGCT | TCCCTAACCA | CCCCTCTTCT | CTTGGCCCAG | CCTGGTTCCC | CCCACTTCCA | 2940 |
| CTCCCCTCTA | CTCTCTCTAG | GACTGGGCTG | ATGAAGGCAC | TGCCCAAAAT | TTCCCCTACC | 3000 |
| CCCAACTTTC | CCCTACCCCC | AACITTTCCC | ACCAGCTCCA | CAACCCTGTT | TGGAGCTACT | 3060 |
| GCAGGACCAG | AAGCACAAAG | TGCGGTTTCC | CAAGCCTTTG | TCCATCTCAG | CCCCCAGAGT | 3120 |
| ATATCTGTGC | TTGGGGAATC | TCACACAGAA | ACTCAGGAGC | ACCCCTTGCC | TGAGCTAAGG | 3180 |
| GAGGTCTTAT | CTCTCAGGGG | GGGTTTAAGT | GCCGTTTGCA | ATAATGTCGT | CTTATTTATT | 3240 |
| TAGCGGGGTG | AATATTTTAT | ACTGTAAGTG | AGCAATCAGA | GTATAATGTT | TATGGTGACA | 3300 |
| AAATTAAAGG | CTTTCTTATA | TGTTTAAAAA | AAAAAAAAAA | AAAAAAAAAA | AAAAAAAAAA | 3360 |
| AAAAAAAAARA | AAAAAAAAAA | AAAAAAAAAA | AAAAAATAA | AAAAAAAAAA | | 3410 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| AGCCAGGCGT | CCCTCTGCCT | GCCCACTCAG | TGGCAACACC | CGGGAGCTGT | TTTGTCTTTT | 60 |
| GTGGAGCCTC | AGCAGTTCCC | TCTTTCAGAA | CTCACTGCCA | AGAGCCCTGA | ACAGGAGCCA | 120 |
| CCATGCAGTG | CTTCAGCTTC | ATTAAGACCA | TGATGATCCT | CTTCAATTTG | CTCATCTTTC | 180 |
| TGTGTGGTGC | AGCCCTGTTG | GCAGTGGGCA | TCTGGGTGTC | AATCGATGGG | GCATCCTTTC | 240 |
| TGAAGATCTT | CGGGCCACTG | TCGTCCAGTG | CCATGCAGTT | TGTCAACGTG | GGCTACTTCC | 300 |
| TCATCGCAGC | CGGCGTTGTG | GTCTTTGCTC | TTGGTTTCCT | GGGCTGCTAT | GGTGCTAAGA | 360 |
| CTGAGAGCAA | GTGTGCCCTC | GTGACGTTCT | TCTTCATCCT | CCTCCTCATC | TTCATTGCTG | 420 |
| AGGTTGCAGC | TGCTGTGGTC | GCCTTGGTGT | ACACCACAAT | GGCTGAGCAC | TTCTTGACGT | 480 |
| TGCTGGTAGT | GCCTGCCATC | AAGAAAGATT | ATGGTTCCCA | GGAAGACTTC | ACTCAAGTGT | 540 |
| GGAACACCAC | CATGAAAGGG | CTCAAGTGCT | GTGGCTTCAC | CAACTATACG | GATTTTGAGG | 600 |
| ACTCACCCCTA | CTTCAAAGAG | AACAGTGCCT | TTCCCCCATT | CTGTTGCAAT | GACAACGTCA | 660 |
| CCAACACAGC | CAATGAAACC | TGCACCAAGC | AAAAGGCTCA | CGACCAAAAA | GTAGAGGGTT | 720 |
| GCTTCAATCA | GCTTTTGTAT | GACATCCGAA | CTAATGCAGT | CACCGTGGGT | GGTGTGGCAG | 780 |
| CTGGAATTGG | GGGCCTCGAG | CTGGCTGCCA | TGATTGTGTC | CATGTATCTG | TACTGCAATC | 840 |
| TACAATAAGT | CCACTTCTGC | CTCTGCCACT | ACTGCTGCCA | CATGGGAACT | GTGAAGAGGC | 900 |
| ACCCTGGCAA | GCAGCAGTGA | TTGGGGGAGG | GGACAGGATC | TAACAATGTC | ACTTGGGCCA | 960 |
| GAATGGACCT | GCCCTTTCTG | CTCCAGACTT | GGGGCTAGAT | AGGGACCACT | CCTTTTAGCG | 1020 |
| ATGCCTGACT | TTCTTCCAT | TGGTGGGTGG | ATGGGTGGGG | GGCATTCCAG | AGCCTCTAAG | 1080 |
| GTAGCCAGTT | CTGTTGCCCA | TTCCCCCAGT | CTATTAAACC | CTTGATATGC | CCCCTAGGCC | 1140 |
| TAGTGGTGAT | CCCAGTGCTC | TACTGGGGGA | TGAGAGAAAG | GCATTTTATA | GCCTGGGCAT | 1200 |
| AAGTGAAATC | AGCAGAGCCT | CTGGGTGGAT | GTGTAGAAGG | CACCTCAAAA | TGCATAAACC | 1260 |
| TGTTACAATG | TTAAAAAATA | AAAAAAAAAA | | | | 1289 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1             5             10             15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20             25             30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
      35             40             45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
      50             55             60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
      65             70             75             80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85             90             95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100            105            110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
      115            120            125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130            135            140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145            150            155            160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165            170            175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180            185            190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
      195            200            205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
      210            215            220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
      225            230            235            240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245            250            255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260            265            270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275            280            285

```

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530

535

540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
50 55 60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65 70 75 80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
85 90 95

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
100 105 110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
115 120 125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
130 135 140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145 150 155 160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
165 170 175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
180 185 190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
195 200 205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
210 215 220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | |
|---|-----|
| GCTCTTTCTC TCCCCTCCTC TGAATTTAAT TCTTTCAACT TGCAATTTGC AAGGATTACA | 60 |
| CATTTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAAAA GTGTCTTTGT TTAAAATTAC | 120 |
| TTGGTTTGTG AATCCATCTT GCTTTTCCC CATTGGAAC AGTCATTAAC CCATCTCTGA | 180 |
| ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT | 240 |
| TCTCAGAAC ATTTCACCCA GACAGCCTGT TTCTATCCTG TTTAATAAAT TAGTTGGGT | 300 |
| TCTCTACATG CATAACAAAC CTTGCTCCAA TCTGTCACAT AAAAGTCTGT GACTTGAAGT | 360 |
| TTAGTC | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|---|-----|
| ACAAAGATGA ACCATTTCTT ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT | 60 |
| GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA | 120 |
| AGACTTTACT ATTTTCATAT TTTAAGACAC ATGATTTATC CTATTTTAGT AACCTGGTTC | 180 |
| ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTGGCAGA AAATCTATGT | 240 |
| TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCT TT | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | |
|---|-----|
| ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA | 60 |
| TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA | 120 |
| AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA | 180 |
| TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGGAA ACAGATGAGG TCACCTCTGT | 240 |
| GACTGCCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT | 300 |
| TGGGT | 305 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | |
|---|----|
| ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGAAAA | 60 |
| AANTCCTGGG T | 71 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|--|-----|
| ACTCCGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA | 60 |
| GAAAATGGGG TGAAATGGC CAACTTCTA TNACTTATG TTGGCAANTT TGCCACCAAC | 120 |
| AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCCTAANC GGAATTAANT | 180 |
| AATGGANTCA AGANACTCCC AGGCCTCAGC GT | 212 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60
CTCCGCCGGC GCAGAACATG CTGGGTGGT 90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTGA 60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTCTTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTGTGTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

| | |
|---|----|
| TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA | 60 |
| TTATCAANTA TTGTGT | 76 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

| | |
|---|-----|
| ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT | 60 |
| CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAT AGCCAATTTT ATTCTCTTGG | 120 |
| TTAAGATTG T | 131 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | |
|---|-----|
| ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG | 60 |
| CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA | 120 |
| CTACAGTCTG CATTTGGCAG AAATGAAGAT GAATTGGAT TAAATGAGGA TGCTGAAGAT | 180 |
| TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG | 240 |
| CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC | 300 |
| CATGGTGGGG GTCTTGCATC TGTAAAGATG GAATTGATT TGCTTTTGCA AGAATCTCAG | 360 |
| CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC | 420 |
| CTCTTTGCTT GT | 432 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | |
|--|-----|
| ACACAACCTG AATAGTAAAA TAGAACTGA GCTGAAATTT CTAATTCCTT TTCTAACCAT | 60 |
| AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT | 112 |

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | |
|---|----|
| ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG | 54 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | |
|---|-----|
| ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTCTCTAA TGTCTCCCCT CTACCAGCTC | 60 |
| ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTCG TCTCTGCTCA | 120 |
| TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC | 180 |
| CCAAAGCATT TGGACAGTTT CTGTTGTGT TTAGAATGG TTTTCTTTT TCTTAGCCTT | 240 |
| TTCTTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT | 300 |
| AGGCTGCCTT CTTTTCATG TCC | 323 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | |
|--|-----|
| ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC | 60 |
| TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTATC | 120 |

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG 180
GATAAACAAA GT 192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTT TTA TGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA 60
TATAATGACG CAACAAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA 120
GTTTCCATTG TGTTTGCGG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA 180
TTCTGTATTC CATTTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA 240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT 300
TGCAGCAGGA AGCACGTGTG GGTGTTGTTG AAAGCTCTTT GCTAATCTTA AAAAGTAATG 360
GG 362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGA AAA GATCGTGTCC ACTCCTGTGG ACATCTTGTT TTAATGGAGT TTCCCATGCA 60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA 120
GTTCTCCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC 180
TTCTGAACTA GATTAAGGCA GCTTGTA AAT CTGATGTGAT TTGGTTTATT ATCCAACTAA 240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC 300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT 332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | |
|---|-----|
| ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC | 60 |
| AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT | 120 |
| CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT | 180 |
| TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG | 240 |
| GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT | 300 |
| GTAACAATCT ACAATTGGTC CA | 322 |

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

| | |
|---|-----|
| ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT | 60 |
| CTTGTTTTTC TTTCCATCTG GTCCTGGGT TGACAATTG TGGAAACAAC TCTATTGCTA | 120 |
| CTATTTAAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCTG | 180 |
| CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTG TTTGATGGGT | 240 |
| CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG | 278 |

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

| | |
|--|-----|
| GTTTANAAAA CTTGTTAGC TCCATAGAGG AAAGAATGTT AAACTTGTA TTTTAAACA | 60 |
| TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTTT TACTTGATT TTGCTTTTG | 120 |
| T | 121 |

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ACTTANAACC | ATGCCTAGCA | CATCAGAATC | CCTCAAAGAA | CATCAGTATA | ATCCTATACC | 60 |
| ATANCAAGTG | GTGACTGGTT | AAGCGTGCGA | CAAAGGTCAG | CTGGCACATT | ACTTGTGTGC | 120 |
| AAACTTGATA | CTTTTGTTC | AAGTAGGAAC | TAGTATACAG | TNCCTAGGAN | TGGTACTCCA | 180 |
| GGGTGCCCCC | CAACTCCTGC | AGCCGCTCCT | CTGTGCCAGN | CCCTGNAAGG | AACTTTTCGCT | 240 |
| CCACCTCAAT | CAAGCCCTGG | GCCATGCTAC | CTGCAATTGG | CTGAACAAAC | GTTTGCTGAG | 300 |
| TTCCCAAGGA | TGCAAAGCCT | GGTGCTCAAC | TCCTGGGGCG | TCAACTCAGT | | 350 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TGTACCGTGA | AGACGACAGA | AGTTGCATGG | CAGGGACAGG | GCAGGGCCGA | GGCCAGGGTT | 60 |
| GCTGTGATTG | TATCCGAATA | NTCCTCGTGA | GAAAAGATAA | TGAGATGACG | TGAGCAGCCT | 120 |
| GCAGACTTGT | GTCTGCCTTC | AANAAGCCAG | ACAGGAAGGC | CCTGCCTGCC | TTGGCTCTGA | 180 |
| CCTGGCGGCC | AGCCAGCCAG | CCACAGGTGG | GCTTCTTCCT | TTTGTGGTGA | CAACNCCAAG | 240 |
| AAACTGCAG | AGGCCCAGGG | TCAGGTGTNA | GTGGGTANGT | GACCATAAAA | CACCAGGTGC | 300 |
| TCCAGGAAC | CCGGGCAAAG | GCCATCCCCA | CCTACAGCCA | GCATGCCAC | TGGCGTGATG | 360 |
| GGTGACAGANG | GATGAAGCAG | CCAGNTGTTC | TGCTGTGGT | | | 399 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| ACTGGTGTGG | TNGGGGGTGA | TGCTGGTGGT | ANAAGTTGAN | GTGACTTCAN | GATGGTGTGT | 60 |
| GGAGGAAGTG | TGTGAACGTA | GGATGTAGA | NGTTTGGCC | GTGCTAAATG | AGCTTCGGGA | 120 |
| TTGGCTGGTC | CCACTGGTGG | TCACTGTCTAT | TGGTGGGGTT | CCTGT | | 165 |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | |
|---|-----|
| ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC | 60 |
| TTAACTTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCCAA | 120 |
| TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG | 180 |
| TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGA GGGCTGGGG CATANANGGT | 240 |
| CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTTGCCAC TGTACATTCC CCATNTTTAA | 300 |
| AAAAACTGAT GCCTTTTTTT TTTTTTTTTG TAAAATTC | 338 |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | |
|--|-----|
| GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA | 60 |
| GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA | 120 |
| ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACC GCC TATCATCTGC | 180 |
| ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG | 240 |
| CCTTATTTGT CTTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT | 300 |
| GTCAGCTATG TGCCCATCC TCCTTCATGC CCTCCCTCCC TTTCTACCA CTGCTGAGTG | 360 |
| GCCTGGA ACT TGTTTAAAGT GT | 382 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|---|-----|
| ACCAAANCTT CTTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT | 60 |
| ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG | 120 |
| TTTTACATT TCAACTGTA TGTGTTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTT | 180 |
| ATATTAGCA TAAAGGAGAA | 200 |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|---|-----|
| ACTTTATTTT CAAACACTC ATATGTTGCA AAAACACAT AGAAAAATAA AGTTTGGTGG | 60 |
| GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT | 120 |
| ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA | 180 |
| AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG | 240 |
| TTTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG | 300 |
| ATTCACAAAC CAAGTAATTT TAAACAAAGA CACTT | 335 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|---|-----|
| ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATTTA | 60 |
| GGGTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT | 120 |
| CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA | 180 |
| CACATGGTCC AACAACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATGGTC | 240 |
| TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCTCCGACA TAAACCACA | 300 |
| TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA | 360 |
| AGCTACCAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT | 420 |
| CAGCANGGT GGGAGGAACC AGCTCAACCT TGGCGTANT | 459 |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|--|-----|
| ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG | 60 |
| AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTCACCA ACCCCACCA TCTCCCTGAG | 120 |
| ACCATCCGAC TTCCCTGTGT | 140 |

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|---|-----|
| AC TTCAGTAA CAACATACAA TAACAACATT AAGTGATAT TGCCATCTTT GTCATTTTCT | 60 |
| ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTTG | 120 |
| AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAG ATGT | 164 |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| ACGTAGACCA TCCAACCTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA | 60 |
| ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT | 120 |
| GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTTGT ATAAACTTCA | 180 |
| GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG | 240 |
| TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT | 300 |
| CAA | 303 |

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|--|-----|
| ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTTCATCANC TTCTCCCTGG GTCCTATGAC | 60 |
| ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTGAGAGA GTCCTTTGC CAACAGGCCT | 120 |
| CCAAGTCAGG GCTGGGATTT GTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT | 180 |
| CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC | 240 |
| AGACTTGCCC CTGGGCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG | 300 |
| TAGGGGTGAG CTGTGTGACT CTATGGT | 327 |

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT | 173 |

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|--|-----|
| ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACACAC TCACTGTGCC TTTCTATCCT | 60 |
| ATGGGATATA TTATTTGATG CTCCATTTCA TCACACATAT ATGAATAATA CACTCATACT | 120 |
| GCCCTACTAC CTGCTGCAAT AATCACAATC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG | 180 |
| GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC | 240 |
| NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA | 300 |
| TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG | 360 |
| CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT | 420 |
| CCAGGCACAG GCTACCTCAT CTTCAACAAT ACCCCTTTAA TTACCATGCT ATGGTG | 477 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC | 60 |
| TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT | 120 |

GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA 180
TTTCAGGCAG AGGGAACAGC AGTGAAA 207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTAGCT AAAACATGGG 60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
GGATACCAAC CGGAAAACCC CTATCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG 180
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATACAGAAC 60
CTTCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | |
|---|-----|
| ACAAACCCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTGAG | 60 |
| CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA | 120 |
| GCACATCAAT AAAGTCCAAA GTCTTGGAAT TGGCCTTGGC TTGGAGGAAG TCATCAACAC | 180 |
| CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGACCA | 240 |
| GTCTGCAGGC CCTGTGAAG CGCCGTCCAC ACGGAGTNAG GAATT | 285 |

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | |
|--|-----|
| ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC | 60 |
| ACCCCAAAT TTTCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC | 120 |
| CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG | 180 |
| ATTGGCACAG GAGTCGAAGG TGTTTCAGTC CCTCTCTCCG TGGAAACGAGA CTCTGATTTG | 240 |
| AGTTTCACAA ATTCTCGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG | 300 |
| GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG | 333 |

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG | 60 |
| GAAAGTGCTT TGGGAAGTGT AAAGTGCTTA ACACATGATC GATGATTTTT GTTATAATAT | 120 |
| TTGAATCAGG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC | 180 |
| ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT | 240 |

GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG 300
GCCCTGGT 308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA 60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA 120
GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT 180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT 240
AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT 295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT 60
GAAGAGCAAA ACAAATCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC 120
CTTAGT 126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTGGAACA CCCATCCTTA ATACGATGAT TTTTCTGTCG TGTGAAATG 60
AANCCAGCAG GCTGCCCTTA GTCAGTCCTT CCTTCAGAG AAAAGAGAT TTGAGAAAGT 120
GCCTGGGTAA TTCACCATTA ATTTCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT 180

| | |
|---|-----|
| CTGGTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA | 240 |
| NATGTTTGTA GCCTTGACATA CTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG | 300 |
| CCAACCCTGT TTTCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA | 360 |
| NACAGACGGG CTCTTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG | 420 |
| TGTTCAATTCT CTGATGTCCT GT | 442 |

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | |
|--|-----|
| ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTT | 60 |
| TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG | 120 |
| GCTGCTGTGG ACTGTTGTTG ATTCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG | 180 |
| GTGTGTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC | 240 |
| TGCTGTGGTG CCGGGANGTG AANGTGTGT GTCACTTGAG CTTGGCCAGC TCTGAAAAGT | 300 |
| ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA | 360 |
| CGAACCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCTN | 420 |
| TCAGGTAANA ATGTGGTTTC AGTGTCCTG GGCNGCTGTG GAAGGTTGTA NATGTCACC | 480 |
| AAGGAATAA GCTGTGGT | 498 |

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|-----|
| ACCTGCATCC AGCTTCCCTG CCAAATCAC AAGGAGACAT CAACCTCTAG ACAGGGAAC | 60 |
| AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT | 120 |
| GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGTCTGA GGAAGCCATT TGAGTCTGGC | 180 |
| CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC | 240 |
| CCACCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG | 300 |
| GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA | 360 |
| CTTGTAAGAT GAAGCCTGGA | 380 |

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTGGCC TTGCCTGTCA    60
CACTGTCCAC TGGCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT      114
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
ACTTTCGAA TCGAATCAAA TGATACTTAG TGTAAGTTTA ATATCCTCAT ATATATCAAA    60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT    120
TGGTGATATA TAACTTGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT      177
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAC GCGAAATTCT ATCCCGTGAC    60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT    120
CATCAGCGGC ATGATGT      137
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|---|-----|
| CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA | 60 |
| TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA | 120 |
| TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT | 180 |
| GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG | 240 |
| GGTTATGACA AAGACAACTG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG | 300 |
| GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT | 360 |
| TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT | 420 |
| GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT | 469 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|---|-----|
| ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTCATA AAGCTGGTGG | 60 |
| ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC | 120 |
| TGCAGGCCGC CCGCCGCTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT | 180 |
| TCCTCTGAGA TGAGT | 195 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|---|-----|
| ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC | 60 |
| CGAGGTCGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT | 120 |
| TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT | 180 |
| TTTGCAGACC AGCCTGAGCA AGGGCCGGAT GTTCAGCTTC AGTCCTCCT TCGTCAGGTG | 240 |
| GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC | 300 |
| GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTCTCTGGG AGCTGCTAGT | 360 |
| NGGGGCCTTT TTGGTGAAC TTT | 383 |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAGAGCCAG | ACCTTGGCCA | TAAATGAANC | AGAGATTAAG | ACTAAACCCC | AAGTCGANAT | 60 |
| TGGAGCAGAA | ACTGGAGCAA | GAAGTGGGCC | TGGGGCTGAA | GTAGAGACCA | AGGCCACTGC | 120 |
| TATANCCATA | CACAGAGCCA | ACTCTCAGGC | CAAGGCNATG | GTTGGGGCAG | ANCCAGAGAC | 180 |
| TCAATCTGAN | TCCAAAGTGG | TGGCTGGAAC | ACTGGTCATG | ACANAGGCAG | TGACTCTGAC | 240 |
| TGANGTC | | | | | | 247 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTCTAAGT | TTTCTAGAAG | TGGAAGGATT | GTANTCATCC | TGAAAATGGG | TTTACTTCAA | 60 |
| AATCCCTCAN | CCTTGTCTT | CACNACTGTC | TATACTGANA | GTGTCATGTT | TCCACAAAGG | 120 |
| GCTGACACCT | GAGCCTGNAT | TTTCACTCAT | CCCTGAGAAG | CCCTTTCCAG | TAGGGTGGGC | 180 |
| AATTCCCAAC | TTCCTTGCCA | CAAGCTTCCC | AGGCTTTCTC | CCCTGGAAAA | CTCCAGCTTG | 240 |
| AGTCCCAGAT | ACACTCATGG | GCTGCCCTGG | GCA | | | 273 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAGCCTTGG | CTTCCCCAAA | CTCCACAGTC | TCAGTGCAGA | AAGATCATCT | TCCAGCAGTC | 60 |
| AGCTCAGACC | AGGGTCAAAG | GATGTGACAT | CAACAGTTTC | TGGTTTCAGA | ACAGGTCTA | 120 |
| CTACTGTCAA | ATGACCCCC | ATACTTCCTC | AAAGGCTGTG | GTAAGTTTTG | CACAGGTGAG | 180 |
| GGCAGCAGAA | AGGGGGTANT | TACTGATGGA | CACCATCTTC | TCTGTATACT | CCACACTGAC | 240 |
| CTTGCCATGG | GCAAAGGCC | CTACCACAAA | AACAATAGGA | TCACTGCTGG | GCACCAGCTC | 300 |
| ACGCACATCA | GTACAACCG | GGATGGAAAA | AGAANTGCCA | ACTTTCATAC | ATCCAAGTGG | 360 |
| AAAGTGATCT | CATACTGGAT | TCTTAATTAC | CTTCAAAAGC | TTCTGGGGGC | CATCAGCTGC | 420 |
| TCGAACACTG | A | | | | | 431 |

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|---|-----|
| ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC | 60 |
| TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT | 120 |
| CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT | 180 |
| GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT | 240 |
| TCAAAGCTAG GGGTCTGGCA GGTGGA | 266 |

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | |
|--|------|
| GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA | 60 |
| CTGGTCATGG AAAACGAATT GTTCTGCTCG GCGTCCTGG TGCATCCGCA GTGGGTGCTG | 120 |
| TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG | 180 |
| CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA | 240 |
| CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC | 300 |
| GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC | 360 |
| GCGGGGAACCT CTGCTCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC | 420 |
| GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC | 480 |
| CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GCGGAGGGC AAGACCAGAA GGACTCCTGC | 540 |
| AACGGTGACT CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAGGGCCT TGTGTCTTTC | 600 |
| GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC | 660 |
| ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AATCCATGAA | 720 |
| ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCT | 780 |
| CCCTCAGGCC CAGGAGTCCA GGCCCCAGC CCCTCCTCCC TCAAACCAAG GTTACAGATC | 840 |
| CCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC | 900 |
| CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC | 960 |
| CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC | 1020 |
| CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA | 1080 |
| GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC | 1140 |
| AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT | 1200 |
| AAGAGAAGNG CAAAAA AAAA AAAAAA AAAAAA | 1248 |

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1             5             10             15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20             25             30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35             40             45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50             55             60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65             70             75             80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85             90             95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100            105            110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115            120            125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130            135            140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145            150            155

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC      60
TCGGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC      120
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG      180
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC      240

```

| | | | | | | |
|-------------|------------|-------------|-------------|------------|------------|------|
| CTCATGCTCA | TCAAGTTGGA | CGAATCCGTG | TCCGAGTCTG | ACACCATCCG | GAGCATCAGC | 300 |
| ATTGCTTCGC | AGTGCCCTAC | CGCGGGGAAC | TCTTGCCCTCG | TTTCTGGCTG | GGGTCTGCTG | 360 |
| GCGAACGGTG | AGCTCACGGG | TGTGTGTCTG | CCCTCTTCAA | GGAGGTCCTC | TGCCCAGTCG | 420 |
| CGGGGGCTGA | CCCAGAGCTC | TGCGTCCCAG | GCAGAAATGCC | TACCGTGCTG | CAGTGCGTGA | 480 |
| ACGTGTCCGT | GGTGTCTGAG | GAGGTCTGCA | GTAAGCTCTA | FGACCCGCTG | TACCACCCCA | 540 |
| GCATGTCTCTG | CGCCGGCGGA | GGGCAAGACC | AGAAGGACTC | CTGCAACGGT | GACTCTGGGG | 600 |
| GGCCCCCTGAT | CTGCAACGGG | TACTTGCAAGG | GCCTTGCTGTC | TTTCGGAAAA | GCCCCGTGTG | 660 |
| GCCAAGTTGG | CGTGCCAGGT | GTCTACACCA | ACCTCTGCAA | ATTCACTGAG | TGGATAGAGA | 720 |
| AAACCGTCCA | GGCCAGTTAA | CTCTGGGGAC | TGGGAACCCA | TGAAATTGAC | CCCCAAATAC | 780 |
| ATCCTGCGGA | AGGAATTCAG | GAATATCTGT | TCCCAGCCCC | TCCTCCCTCA | GGCCCAGGAG | 840 |
| TCCAGGCCCC | CAGCCCCTCC | TCCCTCAAAC | CAAGGGTACA | GATCCCCAGC | CCCTCCTCCC | 900 |
| TCAGACCCAG | GAGTCCAGAC | CCCCCAGCCC | CTCCTCCCTC | AGACCCAGGA | GTCCAGCCCC | 960 |
| TCCTCCNTCA | GACCCAGGAG | TCCAGACCCC | CCAGCCCCTC | CTCCCTCAGA | CCCAGGGGTT | 1020 |
| GAGGCCCCCA | ACCCCTCCTC | CTTCAGAGTC | AGAGGTCCAA | GCCCCCAACC | CCTCGTTCCC | 1080 |
| CAGACCCAGA | GGTNNAGGTC | CCAGCCCCTC | TTCNTCAGA | CCCAGNGGTC | CAATGCCACC | 1140 |
| TAGATTTTCC | CTGNACACAG | TGCCCCCTTG | TGGNANGTTG | ACCCAACCTT | ACCAGTTGGT | 1200 |
| TTTTCATTTT | TNGTCCCTTT | CCCCTAGATC | CAGAAATAAA | GTTTAAGAGA | NGNGCAAAAA | 1260 |
| AAAAA | | | | | | 1265 |

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| GGTCAGCCGC | ACACTGTTTC | CAGAAGTGAG | TGCAGAGCTC | CTACACCATC | GGGCTGGGCC | 60 |
| TGCACAGTCT | TGAGGCCGAC | CAAGAGCCAG | GGAGCCAGAT | GGTGGAGGCC | AGCCTCTCCG | 120 |
| TACGGCACCC | AGAGTACAAC | AGACCCTTGC | TCGCTAACGA | CCTCATGCTC | ATCAAGTTGG | 180 |
| ACGAATCCGT | GTCCGAGTCT | GACACCATCC | GGAGCATCAG | CATTGCTTCG | CAGTGCCCTA | 240 |
| CCGCGGGGAA | CTCTTGCCCTC | GTTTCTGGCT | GGGCTCTGCT | GGCGAACGGT | GAGCTCACGG | 300 |
| GTGTGTGTCT | GCCCTCTTCA | AGGAGGTCCT | CTGCCCAGTC | GCGGGGGCTG | ACCCAGAGCT | 360 |
| CTGCGTCCCA | GGCAGAATGC | CTACCGTGCT | GCAGTGCGTG | AACGTGTCCG | TGGTGTCTGA | 420 |
| NGAGGTCTGC | ANTAAGCTCT | ATGACCCGCT | GTACCACCCC | ANCATGTTCT | GCGCCGGCGG | 480 |
| AGGGCAAGAC | CAGAAGGACT | CCTGCAACGT | GAGAGAGGGG | AAAGGGGAGG | GCAGGCGACT | 540 |
| CAGGGAAGGG | TGGAGAAGGG | GGAGACAGAG | ACACACAGGG | CCGCATGGCG | AGATGCAGAG | 600 |
| ATGGAGAGAC | ACACAGGGAG | ACAGTGACAA | CTAGAGAGAG | AAACTGAGAG | AAACAGAGAA | 660 |
| ATAAACACAG | GAATAAAGAG | AAGCAAAAGG | AGAGAGAAAC | AGAAACAGAC | ATGGGGAGGC | 720 |
| AGAAACACAC | ACACATAGAA | ATGCAGTTGA | CCTTCCAACA | GCATGGGGCC | TGAGGGCGGT | 780 |
| GACCTCCACC | CAATAGAAAA | TCCTCTTATA | ACTTTTGACT | CCCCAAAAAC | CTGACTAGAA | 840 |
| ATAGCCTACT | GTGACGGGG | AGCCTTACCA | ATAACATAAA | TAGTCGATTT | ATGCATACGT | 900 |
| TTTATGCATT | CATGATATAC | CTTTGTTGGA | ATTTTTTGAT | ATTTCTAAGC | TACACAGTTC | 960 |
| GTCTGTGAAT | TTTTTTAAAT | TGTTGCAACT | CTCCTAAAA | TTTTCTGATG | TGTTTATTGA | 1020 |
| AAAAATCCAA | GTATAAGTGG | ACTTGTGCAT | TCAAACACAG | GTTGTTCAAG | GGTCAACTGT | 1080 |
| GTACCCAGAG | GGAAACAGTG | ACACAGATTC | ATAGAGGTGA | AACACGAAGA | GAAACAGGAA | 1140 |
| AAATCAAGAC | TCTACAAAGA | GGCTGGGCAG | GGTGGCTCAT | GCCTGTAATC | CCAGCACTTT | 1200 |
| GGGAGGCGAG | GCAGGCAGAT | CACTTGAGGT | AAGGAGTTCA | AGACCAACCT | GGCCAAAATG | 1260 |
| GTGAAATCCT | GTCTGTACTA | AAAATACAAA | AGTTAGCTGG | ATATGGTGGC | AGGCGCCTGT | 1320 |
| AATCCAGCT | ACTTGGGAGG | CTGAGGCAGG | AGAATTGCTT | GAATATGGGA | GGCAGAGGTT | 1380 |
| GAAGTGAGTT | GAGATCACAC | CACTATACTC | CAGCTGGGGC | AACAGAGTAA | GACTCTGTCT | 1440 |
| CAAAAAA | AAAAA | | | | | 1459 |

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCGCTC GGGCGTCCTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCCTGC ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAATC TTGCCTCGTN TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCCAGCATG TTCTGCGCCG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGCCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTCG GAAAAGCCCC GTGTGGCCAA CTTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCA CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCTCCTC CTCTAGGCC AGGAGTCCAG GCCCCAGCC CCTCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCTC CTCCCTCAGA CCCAGGAGTC CAGACCCCC AGCCCCTCNT      840
CCNTCAGACC CAGGAGTCCA GCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCCCACCCC TCNTCCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC     1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNTCCCTGTA CACAGTGCCC CCTTGTGGCA     1080
NGTTGACCCA ACCTTACCAG TTGGTTTTTC ATTTTGTGTC CCTTCCCCT AGATCCAGAA     1140
ATAAAGTNTA AGAGAAGCGC AAAAAAA
                                                                                   1167
  
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1              5              10              15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20              25              30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35              40              45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
50              55              60
  
```

108

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100 105 110
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GCGCACTCGC | AGCCCTGGCA | GCGGGCACTG | GTCATGGAAA | ACGAATGTT | CTGCTCGGGC | 60 |
| GTCCTGGTGC | ATCCGCACTG | GGTGCTGTCA | GCCGCACACT | GTTTCCAGAA | CTCCTACACC | 120 |
| ATCGGGCTGG | GCCTGCACAG | TCTTGAGGCC | GACCAAGAGC | CAGGGAGCCA | GATGGTGAG | 180 |
| GCCAGCCTCT | CCGTACGGCA | CCCAGAGTAC | AACAGACCCT | TGCTCGCTAA | CGACCTCATG | 240 |
| CTCATCAAGT | TGGACGAATC | CGTGTCCGAG | TCTGACACCA | TCCGGAGCAT | CAGCATTGCT | 300 |
| TGCGAGTGCC | CTACCGCGGG | GAACTCTTGC | CTCGTTTCTG | GCTGGGGTCT | GCTGGCGAAC | 360 |
| GATGCTGTGA | TTGCCATCCA | GTCCCAGACT | GTGGGAGGCT | GGGAGTGTGA | GAAGCTTTCC | 420 |
| CAACCCTGGC | AGGGTTGTAC | CATTTCCGCA | ACTTCCAGTG | CAAGGACGTC | CTGCTGCATC | 480 |
| CTCACTGGGT | GCTCACTACT | GCTCACTGCA | TCACCCGGAA | CACTGTGATC | AACTAGCCAG | 540 |
| CACCATAGTT | CTCCGAAGTC | AGACTATCAT | GATTACTGTG | TTGACTGTGC | TGTCTATTGT | 600 |
| ACTAACCATG | CCGATGTTTA | GGTGAAATTA | GCGTCACTTG | GCCTCAACCA | TCTTGGTATC | 660 |
| CAGTTATCCT | CACTGAATTG | AGATTTCCTG | CTTCAGTGTC | AGCCATTCCC | ACATAATTTT | 720 |
| TGACCTACAG | AGGTGAGGGA | TCATATAGCT | CTTCAAGGAT | GCTGGTACTC | CCCTCACAAA | 780 |
| TTCAATTCTC | CTGTTGTAGT | GAAAGGTGCG | CCCTCTGGAG | CCTCCAGGG | TGGGTGTGCA | 840 |
| GGTCACAATG | ATGAATGTAT | GATCGTGTTC | CCATTACCCA | AAGCCTTTAA | ATCCCTCATG | 900 |
| CTCAGTACAC | CAGGGCAGGT | CTAGCATTTT | TTCATTAGT | GTATGCTGTC | CATTATGCA | 960 |
| ACCACCTCAG | GACTCCTGGA | TTCTCTGCCT | AGTTGAGCTC | CTGCATGCTG | CCTCCTTGGG | 1020 |
| GAGGTGAGGG | AGAGGGCCCA | TGGTTCAATG | GGATCTGTGC | AGTTGTAACA | CATTAGGTGC | 1080 |

TTAATAAACA GAAGCTGTGA TGTAAAAA AAAAAAAA

1119

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1             5             10             15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20             25             30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35             40             45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50             55             60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65             70             75             80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85             90             95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100            105            110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115            120            125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130            135            140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145            150            155            160
Pro Gly Thr Leu

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT

60

CCAGCTGCCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT 120
 GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGGCAAGCG CTTCCTGCTGA 180
 AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA 240
 AAAAAAAAAA 250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA 60
 TCACCCAGAC CCCGCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA 120
 CTCTGCTACT CGGAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGT TATAAATGCC 180
 TGATTTAAAA AAAAAAAAAA AA 202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG 60
 AATGTTTAGG CAGTGCTAGT AATTTCTYTCG TAATGATTCT GTTATTACTT TCCTNATTCT 120
 TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA 180
 GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA 240
 AAATATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC 300
 CTACTCTGTT CCTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GGGAAGCCAA 360
 ATTGATAATA TTCTATGTTC TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW 420
 TTTTATTCCC AGGAATATGG KGTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT 480
 AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTT 540
 CAAAAAAAAA AAAAAAAA 558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTK GRGGATGCTA AGSCCCCRGA RWTYGTGTTGA TCCAACCCTG GCTTWTTTTT 60
 AGAGGGGAAA ATGGGGGCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG 120
 CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG 180
 TTWGCAATTC ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA 240
 CTAAGGTAA ACTTTCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA 300
 TACTMTTCTA AGTCTCTTTC CAGCCTCACT KKGAGTCTTM CYTGGGGGTT GATAGGAANT 360
 NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTTGG TACGCATARA 420

AWTGSTGARA AAATTAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAA AAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | |
|---|-----|
| AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC | 60 |
| AGTACCAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCAGTGCT | 120 |
| GGTGCCAGCC TGACCGCCAC TCTCACATTT GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT | 180 |
| GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTCCTCCT ACAAGTGAGA TTTAGATAT | 240 |
| TGTTAATCCT GCCAGTCTTT CTCTTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA | 300 |
| CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT | 360 |
| GCCATTTCAA AAAAAAAAAA AAAA | 384 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

| | |
|--|-----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYTNT CCRGTATKAC CTCAACGAGC | 60 |
| AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG | 120 |
| CCCATCCTGC TCGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA | 180 |
| AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC | 240 |
| TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG | 300 |
| TGAGCCCTGA TGCCTTTTGG CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCGATTG | 360 |
| ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGGAACAC ATTTGACTTT | 420 |
| TTTTTCTCAT ATTTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAACTST | 480 |
| TAAAAAAAAA AAAAAA | 496 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | |
|---|-----|
| GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGAATTCC | 60 |
| CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC | 120 |
| AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT | 180 |
| GGGCACACC TCCTGGGGCC CAGGCGGGCA CTGCGTCTC CCAGTATGCC AACTGGCTGG | 240 |
| TGGTGCTGCT CCTCGTCATC TTCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA | 300 |
| TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG | 360 |
| GCGCAGCGTT ACCGCCTCAT CCGG | 384 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGTTAGCTC | CTCCACAACC | TTGATGAGGT | CGTCTGCAGT | GGCCTCTCGC | TTCATACCGC | 60 |
| TNCCATCGTC | ATACTGTAGG | TTTGCCACCA | CYTCTGGCA | TCTTGGGGCG | GCNTAATATT | 120 |
| CCAGGAAACT | CTCAATCAAG | TCACCGTCGA | TGAAACCTGT | GGGCTGGTTC | TGTCTTCCGC | 180 |
| TCGGTGTGAA | AGGATCTCCC | AGAAGGAGTG | CTCGATCTTC | CCCACACTTT | TGATGACTTT | 240 |
| ATTGAGTCGA | TTCTGCATGT | CCAGCAGGAG | GTTGTACCAG | CTCTCTGACA | GTGAGGTCAC | 300 |
| CAGCCCTATC | ATGCCGTGTA | MCGTGCCGAA | GARCACCGAG | CCTTGTGTGG | GGGKKGAAGT | 360 |
| CTCACCCAGA | TTCTGCATTA | CCAGAGAGCC | GTGGCAAAAG | ACATTGACAA | ACTCGCCAG | 420 |
| GTGGAAAAAG | AMCAMCTCCT | GGARGTGCTN | GCCGCTCCTC | GTCMGTGGT | GGCAGCGCTW | 480 |
| TCCTTTTGAC | ACACAAACAA | GTAAAGGCA | TTTTCAGCCC | CCAGAAANTT | GTCATCATCC | 540 |
| AAGATNTCGC | ACAGCACTNA | TCCAGTTGGG | ATTAAAT | | | 577 |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AACATCTTCC | TGTATAATGC | TGTGTAATAT | CGATCCGATN | TTGTCTGSTG | AGAATYCATW | 60 |
| ACTKGGAAAA | GMAACATTAA | AGCCTGGACA | CTGGTATTAA | AATTCACAA | ATGCAACACT | 120 |
| TTAAACAGTG | TGTCAATCTG | CTCCCYYNAC | TTTGTCTATCA | CCAGTCTGGG | AAKAAGGGTA | 180 |
| TGCCCTATTC | ACACCTGTTA | AAAGGGCGCT | AAGCATTTTT | GATTCAACAT | CTTTTTTTTT | 240 |
| GACACAAGTC | CGAAAAAAGC | AAAAGTAAAC | AGTTATYAAT | TTGTTAGCCA | ATTCACCTTC | 300 |
| TTATGGGAC | AGAGCCATYT | GATTAAAAAA | GCAAATTGCA | TAATATTGAG | CTTYGGGAGC | 360 |
| TGATATTTGA | GCGGAAGAGT | AGCCTTTCTA | CTTCACCAGA | CACAACTCCC | TTTCATATTG | 420 |
| GGATGTTNAC | NAAAGTWATG | TCTCTWACAG | ATGGGATGCT | TTTGTGGCAA | TTCTGTTCTG | 480 |
| AGGATCTCCC | AGTTTATTTA | CCACTTGCAC | AAGAAGGCGT | TTTCTTCCTC | AGGC | 534 |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| AGAAACCAGT | ATCTCTNAAA | ACAACCTCTC | ATACCTTGTG | GACCTAATTT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTTT | TACTTTTGTA | AAAGCTTATG | 120 |
| CCTCTTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTCAA | TCTAGTTNGT | 240 |
| TTTATTCGAC | ATGAAGGAAA | TTCCAGATN | ACAACACTNA | CAAACTCTCC | CTKGACKARG | 300 |
| GGGGACAAAG | AAAAGCAAAA | CTGAMCATAA | RAAACAATWA | CCTGGTGAGA | ARTTGACATAA | 360 |
| ACAGAAATWR | GGTAGTATAT | TGAARNACAG | CATCATTAATA | RMGTTWTKTT | WTTCTCCCTT | 420 |

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|-----|
| GCAAAAAACA | TGTACNGACT | TCCCCTTGAG | TAATGCCAAG | TTGTTTTTTT | TATNATAAAA | 480 |
| CTTGCCCTTC | ATTACATGTT | TNAAAGTGGT | GTGGTGGGCC | AAAATATTGA | AATGATGGAA | 540 |
| CTGACTGATA | AAGCTGTACA | AATAAGCAGT | GTGCCTAACA | AGCAACACAG | TAATGTTGAC | 600 |
| ATGCTTAATT | CACAAATGCT | AATTTTCATTA | TAAATGTTTG | CTAAAATACA | CTTTGAACTA | 660 |
| TTTTTCTGTN | TCCCCAGAGC | TGAGATNTTA | GATTTTATGT | AGTATNAAGT | GAAAAANTAC | 720 |
| GAAAAATAATA | ACATTGAAGA | AAAANANAAA | AAANAAAAAA | A | | 761 |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTGCCGATN | CTACTATTTT | ATTGCAGGAN | GTGGGGGTGT | ATGCACCGCA | 60 |
| CACCGGGGCT | ATNAGAAGCA | AGAAGGAAGG | AGGGAGGGCA | CAGCCCCCTG | CTGAGCAACA | 120 |
| AAGCCGCCTG | CTGCCCTCTC | TGTCTGTCTC | CTGGTGCAGG | CACATGGGGA | GACCTTCCCC | 180 |
| AAGGCAGGGG | CCACCACTCC | AGGGGTGGGA | ATACAGGGGG | TGGGANGTGT | GCATAAGAAG | 240 |
| TGATAGGCAC | AGGCCACCCG | GTACAGACCC | CTCGGCTCCT | GACAGGTNGA | TTTCGACCAG | 300 |
| GTCATTGTGC | CCTGCCCAGG | CACAGCGTAN | ATCTGGAAAA | GACAGAATGC | TTTCCTTTTC | 360 |
| AAATTTGGCT | NGTCATNGAA | NGGGCANTTT | TCCAANTTNG | GCTNGGTCTT | GGTACNCTTG | 420 |
| GTTTCGGCCA | GCTCCNCGTC | CAAAAANTAT | TCACCCNNCT | CCNAATTGCT | TGCNGGNCCC | 480 |
| CC | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTAAAAACA | GTTTTTCACA | ACAAAATTTA | TTAGAAGAAT | AGTGGTTTTG | 60 |
| AAAACCTCTG | CATCCAGTGA | GAACTACCAT | ACACCACATT | ACAGCTNGGA | ATGTNCTCCA | 120 |
| AATGTCTGGT | CAAATGATAC | AATGGAACCA | TTCAATCTTA | CACATGCACG | AAAGAACAAG | 180 |
| CGCTTTTGAC | ATACAATGCA | CAAAAAAAAA | AGGGGGGGGG | GACCACATGG | ATTAAAATTT | 240 |
| TAAGTACTCA | TCACATACAT | TAAGACACAG | TTCTAGTCCA | GTCAAAAATC | AGAACTGCNT | 300 |
| TGAAAAATTT | CATGTATGCA | ATCCAACCAA | AGAACTTNAT | TGGTGATCAT | GANTNCTCTA | 360 |
| CTACATCNAC | CTTGATCATT | GCCAGGAACN | AAAAGTTNAA | ANCACNCNGT | ACAAAAANAA | 420 |
| TCTGTAATTN | ANTTCAACCT | CCGTACNGAA | AAATNTTNTT | TATACACTCC | C | 471 |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAGGGATTGA | AGGTCTGTTC | TASTGTCGGM | CTGTTTCAGCC | ACCAACTCTA | ACAAGTTGCT | 60 |
| GTCTTCCACT | CACTGTCTGT | AAGCTTTTTA | ACCCAGACWG | TATCTTCATA | AATAGAACAA | 120 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ATTCTTCACC | AGTCACATCT | TCTAGGACCT | TTTTGGATTC | AGTTAGTATA | AGCTCTTCCA | 180 |
| CTTCCTTTGT | TAAGACTTCA | TCTGGTAAAG | TCTTAAGTTT | TGTAGAAAGG | AATTYAATTG | 240 |
| CTCGTTCTCT | AACAAATGTCC | TCTCCTTGAA | GTATTTGGCT | GAACAACCCA | CCTAAAGTCC | 300 |
| CTTTGTGCAT | CCATTTTAAA | TATACTTAAT | AGGGCATTGK | TNCACTAGGT | TAAATTCTGC | 360 |
| AAGAGTCATC | TGTCTGCAAA | AGTTGCGTTA | GTATATCTGC | CA | | 402 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAGCTCGGAT | CCAATAATCT | TTGTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT | 60 |
| GGTCTACCCC | ACATGGGAGC | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC | 120 |
| ATGCYTYTTT | GAYTACCGTG | TGCCAAGTGC | TGGTGAT'TCT | YAACACACYT | CCATCCCGYT | 180 |
| CTTTTGTGGA | AAACTGGCA | CTTKTCTGGA | ACTAGCARGA | CATCACTTAC | AAATTCAACC | 240 |
| ACGAGACACT | TGAAAGGTGT | AACAAAGCGA | YTCTTGCAAT | GCTTTTTGTC | CCTCCGGCAC | 300 |
| CAGTTGTCAA | TACTAACCCG | CTGGTTTGCC | TCCATCATAT | TGTGTATCTG | TAGCTCTGGA | 360 |
| TACATCTCCT | GACAGTACTG | AAGAACTTCT | TCTTTTGTTT | CAAAAGCARG | TCTTGGTGCC | 420 |
| TGTTGGATCA | GGT'PCCCAT | TCCCAGTCYG | AATGTTTACA | TGGCATATTT | WACTTCCCAC | 480 |
| AAAACATTGC | GATTTGAGGC | TCAGCAACAG | CAAATCCTGT | TCCGGCATTG | GCTGCAAGAG | 540 |
| CCTCGATGTA | GCCGGCCAGC | GCCAAGGCAG | GCGCCGTGAG | CCCCACCAGC | AGCAGAAGCA | 600 |
| G | | | | | | 601 |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| ATACAGCCCA | NATCCCACCA | CGAAGATGCG | CTTGTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCGCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGGTTGATGC | TGCACTCYTT | 120 |
| CCCAACGCAG | GCAGMAGCGG | GS'CCGGTCAA | TGAACTCCAY | TCGTGGCTTG | GGG'KGACGG | 180 |
| TKAAGTG'GAG | GAAGAGGCTG | ACCACCTCGC | GGTCCACCAG | GATGCCCCGAC | TGTGCGGGAC | 240 |
| CTGCAGCGAA | ACTCCTCGAT | GGTCATGAGC | GGGAAGCGAA | TGAGGCC'GAG | GGCCTTGCCC | 300 |
| AGAACCTTCC | GCCTGTTCTC | TGGCGTCACC | TGCAGCTGCT | GCCGCTGACA | CTCGGCCTCG | 360 |
| GACCAGCGGA | CAAACGGC'RT | TGAACAGCCG | CACCTCACGG | ATGCCCAGTG | TGTCGCGCTC | 420 |
| CAGGAMMGSC | ACCAGCGTGT | CCAGGTCAAT | GTCGGTGAAG | CCCTCCGCGG | GTRATGGCGT | 480 |
| CTGCAGTGTT | TTTGTCGATG | TTCTCCAGGC | ACAGGCTGGC | CAGCTGCGGT | TCATCGAAGA | 540 |
| GTCGCGCCTG | CGTGAGCAGC | ATGAAGGCGT | TGTCGGCTCG | CAGTTCTTCT | TCAGGA'ACTC | 600 |
| CACGCAAT | | | | | | 608 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAACGGCTGG | ACCTTGCTC | GCATTGTGCT | TGCTGGCAGG | GAATACCTTG | GCAAGCAGYT | 60 |
| CCAGTCCGAG | CAGCCCCAGA | CCGCTGCCGC | CCGAAGCTAA | GCCTGCCTCT | GGCCTTCCCC | 120 |
| TCCGCCTCAA | TGCAGAACCA | GTAGTGGGAG | CACTGTGTTT | AGAGTTAAGA | GTGAACACTG | 180 |
| TTTGATTTTA | CTTGGGAATT | TCCTCTGTTA | TATAGCTTTT | CCCAATGCTA | ATTTCCAAAC | 240 |
| AACAACAACA | AAATAACATG | TTTGCCTGTT | AAGTTGTATA | AAAGTAGGTG | ATTCTGTATT | 300 |
| TAAAGAAAAT | ATTACTGTTA | CATATACTGC | TTGCAATTTC | TGTATTTATT | GKTNCTSTGG | 360 |
| AAATAAATAT | AGTTATTAAA | GGTTGTCANT | CC | | | 392 |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCSTTKGAGG | GGTKAGGKYC | CAGTTYCCGA | GTGGAAGAAA | CAGGCCAGGA | GAAGTGCCTG | 60 |
| CCGAGCTGAG | GCAGATGTTT | CCACAGTGAC | CCCCAGAGCC | STGGGSTATA | GTYTCTGACC | 120 |
| CCTCNCAAGG | AAAGACCACS | TTCTGGGGAC | ATGGGCTGGA | GGGCAGGACC | TAGAGGCACC | 180 |
| AAGGGAAGGC | CCCATTCGGG | GGSTGTTCCC | CGAGGAGGAA | GGGAAGGGGC | TCTGTGTGCC | 240 |
| CCCCASGAGG | AAGAGGCCCT | GAGTCCTGGG | ATCAGACACC | CCTTCACGTG | TATCCCCACA | 300 |
| CAAATGCAAG | CTACCAAGG | TCCCCTCTCA | GTCCCCTTCC | STACACCCTG | AMCGGCCACT | 360 |
| GSCSCACACC | CACCCAGAGC | ACGCCACCCG | CCATGGGGAR | TGTGCTCAAG | GARTCGCNGG | 420 |
| GCARCCTGGA | CATCTNGTCC | CAGAAGGGGG | CAGAATCTCC | AATAGANGGA | CTGARCMSTT | 480 |
| GCTNANAAAA | AAAAANAAAA | AA | | | | 502 |

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACCATT | TTGTCTGCTC | 60 |
| CCTCTGGAAG | CCTTGCGCAG | AGCGGACTTT | GTAATGTTG | GAGAATAACT | GCTGAATTTT | 120 |
| WAGCTGTTTK | GAGTTGATTS | GCACCACTGC | ACCCACAAC | TCAATATGAA | AACYAWTTGA | 180 |
| ACTWATTTAT | TATCTTGTTA | AAAGTATAAC | AATGAAAATT | TTGTTCATAC | TGTATTKATC | 240 |
| AAGTATGATG | AAAAGCAAWA | GATATATATT | CTTTTATTAT | GTTAAATTAT | GATTGCCATT | 300 |
| ATTAATCGGC | AAAATGTGGA | GTGTATGTTT | TTTTACAGT | AATATATGCC | TTTTGTAACT | 360 |
| TCACTTGGTT | ATTTTATTGT | AAATGARTTA | CAAAATTCTT | AATTTAAGAR | AATGGTATGT | 420 |
| WATATTTAT | TCATTAATTT | CTTTCCTKGT | TTACGTWAAT | TTTGAAAAGA | WTGCATGATT | 480 |
| TCTTGACAGA | AATCGATCTT | GATGCTGTGG | AAGTAGTTTG | ACCCACATCC | CTATGAGTTT | 540 |
| TTCTTAGAAT | GTATAAAGGT | TGTAGCCCAT | CNAACTTCAA | AGAAAAAAAT | GACCACATAC | 600 |
| TTTGCAATCA | GGCTGAAATG | TGGCATGCTN | TTCTAATTCC | AACTTTATAA | ACTAGCAAAN | 660 |
| AAGTG | | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTNTTTTT | TTTTTTTGC | AGGAAGGATT | CCATTATTG | TGGATGCATT | TTCACAATAT | 60 |
| ATGTTTATTG | GAGCGATCCA | TTATCAGTGA | AAAGTATCAA | GTGTTTATAA | NATTTTtagg | 120 |
| AAGGCAGATT | CACAGAACAT | GCTNGTCNGC | TTGCAGTTTT | ACCTCGTANA | GATNACAGAG | 180 |
| AATTATAGTC | NAACCAGTAA | ACNAGGAATT | TACTTTTCAA | AAGATTAAAT | CCAAACTGAA | 240 |
| CAAAATTCTA | CCCTGAAACT | TACTCCATCC | AAATATTGGA | ATAANAGTCA | GCAGTGATAC | 300 |
| ATTCTCTTCT | GAACTTTAGA | TTTTCTAGAA | AAATATGTAA | TAGTGATCAG | GAAGAGCTCT | 360 |
| TGTTCAAAAG | TACAACNAAG | CAATGTTCCC | TTACCATAGG | CCTTAATTCA | AACTTTGATC | 420 |
| CATTTCACCTC | CCATCACGGG | AGTCAATGCT | ACCTGGGACA | CTTGATTTT | GTTCATNCTG | 480 |
| ANCNTGGCTT | AA | | | | | 492 |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTNTTTTGN | ATTTCANTCT | GTANNAANTA | TTTTCATTAT | GTTTATTANA | AAAATATNAA | 60 |
| TGNTCCACN | ACAAATCATN | TTACNTNAGT | AAGAGGCCAN | CTACATTGTA | CAACATACAC | 120 |
| TGAGTATATT | TTGAAAAGGA | CAAGTTTAAA | GTANACNCAT | ATTGCCGANC | ATANCACATT | 180 |
| TATACATGGC | TTGATTGATA | TTTAGCACAG | CANAACTGA | GTGAGTTACC | AGAAANAAAT | 240 |
| NATATATGTC | AATCNGATTT | AAGATACAAA | ACAGATCCTA | TGGTACATAN | CATCNTGTAG | 300 |
| GAGTTGTGGC | TTTATGTTTA | CTGAAAGTCA | ATGCAGTTCC | TGTACAAAGA | GATGGCCGTA | 360 |
| AGCATTCTAG | TACCTCTACT | CCATGGTTAA | GAATCGTACA | CTTATGTTTA | CATATGTNCA | 420 |
| GGGTAAGAAT | TGTGTTAAGT | NAANTTATGG | AGAGGTCCAN | GAGAAAAATT | TGATNCAA | 478 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTGAG | TTTCTCTAC | GGATGAGAGA | CTGGCTCAAG | AATATCTCA | TGCAGCTTTA | 240 |
| TGAAGCCNAC | TCTGAACACG | CTGGTTATCT | NAGATGAGAA | NCAGAGAAAT | AAAGTCNAGA | 300 |
| AAATTTACCT | GGANGAAAAG | AGGCTTTNGG | CTGGGGACCA | TCCCATTGAA | CCTTCTCTTA | 360 |
| ANGGACTTTA | AGAANAACT | ACCACATGTN | TGTNGTATCC | TGGTGCCNGG | CCGTTTANTG | 420 |
| AACNTNGACN | NCACCCTTNT | GGAATANANT | CTTGACNGCN | TCCTGAACTT | GCTCCTCTGC | 480 |
| GA | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC | 60 |
| CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC | 120 |
| AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCAC GACCTTGACG CCGTCGGGGA | 180 |
| CAGCCGGAAC AGAGCCCGGT GAANGCGGA GGCCTCGGG AGCCCTCGG GAAGGGCGGC | 240 |
| CCGAGAGATA CGCAGGTGCA GGTGGCCGCC | 270 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | |
|---|-----|
| TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA | 60 |
| GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCTAG GTCAACTTCC TTGTCTGTGG | 120 |
| TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGG AAANCGAAGC ANAANTAACA | 180 |
| TGGAGTGGGT GCACCCTCCC TGTAGAACCT GGTACNAAA GCTTGGGGCA GTTCACCTGG | 240 |
| TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG | 300 |
| TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAA ATCCACNTGA | 360 |
| AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA | 419 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | |
|---|-----|
| TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT | 60 |
| TGGCACTTAA TCCATTTTTA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATACNG | 120 |
| GTNATTTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAAAATNNA | 180 |
| TACNCNCAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAATAA | 240 |
| AATATATACG GCTGGTGT TTCAAAGTACA ATTATCTTAA CACTGCAAAC ATNTTTNNAA | 300 |
| GGAATAAAA TAAAAAAA CACTNCCGCA AAGGTTAAAG GGAACAACAA ATTCNTTTTA | 360 |
| CAACANCNNC NATTATAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTACACNG | 420 |
| GGATCTTAAC TTTTACTNCA CTTTGTATAT TTTTANAA CCATTGTNTT GGGCCCAACA | 480 |
| CAATGGNAAT NCCNCCNCNC TGGACTAGT | 509 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| TTTTTTTTTT | TTTTTTTGA | CCCCCTCTT | ATAAAAAACA | AGTTACCATT | TTATTTTACT | 60 |
| TACACATATT | TATTTTATAA | TTGGTATTAG | ATATTCAAAA | GGCAGCTTTT | AAAATCAAAC | 120 |
| TAAATGGA | CTGCCCTAGA | TACATAATTC | TTAGGAATTA | GCTTAAAAATC | TGCCTAAAGT | 180 |
| GAAAACTCTC | TCTAGCTCTT | TTGACTGTAA | ATTTTGTACT | CTTGTA AAC | ATCCAAATTC | 240 |
| ATTTTCTCTG | TCTTTAAAAT | TATCTAATCT | TTCCATTTT | TCCCTATTCC | AAGTCAATTT | 300 |
| GCTTCTCTAG | CCTCATTTCC | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT | TTTTCCTAAA | 360 |
| AGGGAAAAACA | GGAAGAGANA | ATGGCACACA | AAACAAACAT | TTTATATTCA | TATTTCTACC | 420 |
| TACGTTAATA | AAATAGCATT | TTGTGAAGCC | AGCTCAAAAG | AAGGCTTAGA | TCCTTTTATG | 480 |
| TCCATTTTAG | TCACTAAACG | ATATCNAAAG | TGCCAGAATG | CAAAAGGTTT | GTGAACATTT | 540 |
| ATTCAAAAGC | TAATATAAGA | TATTTACAT | ACTCATCTTT | CTG | | 583 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTNT | TTTTTTTTTT | TTTTTNCTC | TTCTTTTTTT | TTGANAATGA | GGATCGAGTT | 60 |
| TTTCACTCTC | TAGATAGGGC | ATGAAGAAAA | CTCATCTTTC | CAGCTTTAAA | ATAACAATCA | 120 |
| AATCTCTTAT | GCTATATCAT | ATTTTAAGTT | AACTAATGA | GTCCTGGCT | TATCTTCTCC | 180 |
| TGAAGGAAAT | CTGTTTCTC | TTCTCATTCA | TATAGTTATA | TCAAGTACTA | CCTTGCATAT | 240 |
| TGAGAGGTTT | TTCTTCTCTA | TTTACACATA | TATTTCCATG | TGAATTTGTA | TCAAACCTTT | 300 |
| ATTTTTCATGC | AAACTAGAAA | ATAATGTNTT | CTTTTGCATA | AGAGAAGAGA | ACAATATNAG | 360 |
| CATTACAAAA | CTGCTCAAAT | TGTTTGTAA | GNTTATCCAT | TATAATTAGT | TNGGCAGGAG | 420 |
| CTAATACAAA | TCACATTTAC | NGACNAGCAA | TAATAAACT | GAAGTACCAG | TTAAATATCC | 480 |
| AAAATAATTA | AAGGAACATT | TTTAGCCTGG | GTATAATTAG | CTAATTCACT | TTACAAGCAT | 540 |
| TTATTNAGAA | TGAATTCACA | TGTTATTATT | CCNTAGCCCA | ACACAATGG | | 589 |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTNTTTT | TTTTTTCAGT | AATAATCAGA | ACAATATTTA | TTTTTATATT | TAAAATTCAT | 60 |
| AGAAAAGTGC | CTTACATTTA | ATAAAAGTTT | GTTTCTCAAA | GTGATCAGAG | GAATTAGATA | 120 |
| TNGTCTTGAA | CACCAATATT | AATTTGAGGA | AAATACACCA | AAATACATTA | AGTAAATTAT | 180 |
| TTAAGATCAT | AGAGCTTGTA | AGTGAAAAGA | TAAAATTGTA | CCTCAGAAAC | TCTGAGCATT | 240 |
| AAAAATCCAC | TATTAGCAAA | TAAATTACTA | TGGACTTCTT | GCTTTAATTT | TGTGATGAAT | 300 |
| ATGGGGTGTC | ACTGGTAAAC | CAACACATT | TGAAGGATAC | ATTACTTAGT | GATAGATTCT | 360 |
| TATGTACTTT | GCTANATNAC | TGGGATATGA | GTTGACAAGT | TTCTCTTTCT | TCAATCTTTT | 420 |
| AAGGGGNGA | NGAAATGAGG | AAGAAAAGAA | AAGGATTACG | CATACTGTTC | TTTCTATNGG | 480 |
| AAGGATTAGA | TATGTTTCCT | TTGCCAATAT | TAAAAAATA | ATAATGTTTA | CTACTAGTGA | 540 |
| AACCC | | | | | | 545 |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
TTTTTTTTTT TTTT TAGTC AAGTTCTNA TTTTATTAT AATTAAAGTC TTGGTCATTT      60
CATTATTAG CTCTGCAACT TACATATTTA AATTAAAGAA ACGTTNTTAG ACAACTGTNA      120
CAATTTATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT      180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTTA ATTTTATTAG TAGATNATAC      240
ACTGCTGCAA ACGCTAATTC TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG      300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT      360
TCGGTGAAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG      420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATTT GTGGCNTCTN TTGCACTTGT      480
TTCAAAA                                           487
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```
TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAA      60
TACATAGCAT TAAATCCCAA ATCCTATTTA AAGACCTGAC AGCTTGAGAA GGTCACTACT      120
GCATTATAG GACCTTCTGG TGGTCTGCT GTTACNTTGT AANTCTGACA ATCCTTGANA      180
ATCTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTTCA CAGAGGAANA ACACAGCGCA      240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG      300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA                                           332
```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
AGGGCGTGGT GCGGAGGGCG TTA CTGTTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG      60
GTTGTGTTCC GGCCCCATCC AACCACGAAG TTGATTTCTC TTGTGTGCAG AGTGA CTGAT      120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC      180
TCCCGCGTGA TTCACATTTA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAATACT      240
TTTGGCAGAA TACTTNTTGA AACTTGCAGA TGATAACTAA GATCCAAGAT ATTTCCCAAA      300
GTAAATAGAA GTGGGCATA ATATTAATTA CCTGTTTACA TCAGCTTCCA TTACAAGTC      360
ATGAGCCCAG AACTGACAT CAAACTAAGC CCACTTAGAC TCCTCACCAC CAGTCTGTCC      420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTTCTCA CCAGTCAATC ATCTATCCAA      480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA                                           524
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | |
|---|-----|
| GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG | 60 |
| TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA | 120 |
| CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA | 159 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | |
|---|-----|
| ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC | 60 |
| ACTGAATTC TTTCCTCTG GACTATTACA TGCCANTGA GGGACTAATG GAAAAACGTA | 120 |
| TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT | 180 |
| TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA | 240 |
| CCAGGATGCT AAATCA | 256 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|---|-----|
| ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA | 180 |
| GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA | 240 |
| AAAAAAGGAG CAAATGAGAA GCCT | 264 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ACCCAAAAAT | CCAATGCTGA | ATATTTGGCT | TCATTATTCC | CANATTCTTT | GATTGTCAAA | 60 |
| GGATTTAATG | TTGTCTCAGC | TTGGGCACTT | CAGTTAGGAC | CTAAGGATGC | CAGCCGGCAG | 120 |
| GTTTATATAT | GCAGCAACAA | TATTCAAGCG | CGACAACAGG | TTATTGAACT | TGCCCCGCCAG | 180 |
| TTNAATTTC | TTCCCATGGA | CTTGGGATCC | TTATCATCAG | CCAGAGAGAT | TGAAAATTTA | 240 |
| CCCCTACNAC | TCTTTACTCT | CTGGANAGGG | CCAGTGGTGG | TAGCTATAAG | CTTGGCCACA | 300 |
| TTTTTTTTTC | CTTTATTCTT | TTGTCAGA | | | | 328 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| ACTTATGAGC | AGAGCGACAT | ATCCNAGTGT | AGACTGAATA | AAACTGAATT | CTCTCCAGTT | 60 |
| TAAAGCATTG | CTCACTGAAG | GGATAGAAGT | GACTGCCAGG | AGGGAAAAGTA | AGCCAAGGCT | 120 |
| CATTATGCCA | AAGGANATAT | ACATTTCAAT | TCTCCAAACT | TCTTCCTCAT | TCCAAGAGTT | 180 |
| TTCAATATTT | GCATGAACCT | GCTGATAANC | CATGTTAANA | AACAAATATC | TCTCTNACCT | 240 |
| TCTCATCGGT | | | | | | 250 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| ACCCAGAATC | CAATGCTGAA | TATTTGGCTT | CATTATTCCC | AGATTCTTTG | ATTGTCAAAG | 60 |
| GATTTAATGT | TGTCTCAGCT | TGGGCACTTC | AGTTAGGACC | TAAGGATGCC | AGCCGGCAGG | 120 |
| TTTATATATG | CAGCAACAAT | ATTCAAGCGC | GACAACAGGT | TATTGAACTT | GCCCGCCAGT | 180 |
| TGAATTTTCAT | TCCCATTTGAC | TTGGGATCCT | TATCATCAGC | CANAGAGATT | GAAAATTTAC | 240 |
| CCCTACGACT | CTTTACTCTC | TGGAGAGGGC | CAGTGGTGGT | AGCTATAAGC | TTGGCCACAT | 300 |
| TTTTTTTTTC | TTTATTCCTT | TGTCAGAGAT | GCGATTCATC | CATATGCTAN | AAACCAACAG | 360 |
| AGTGACTTTT | ACAAAATTCC | TATAGANATT | GTGAATAAAA | CCTTACCTAT | AGTTGCCATT | 420 |
| ACTTTGCTCT | CCCTAATATA | CCTC | | | | 444 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| ACTTATGAGC | AGAGCGACAT | ATCCAAGTGT | ANACTGAATA | AAACTGAATT | CTCTCCAGTT | 60 |
| TAAAGCATTG | CTCACTGAAG | GGATAGAAGT | GACTGCCAGG | AGGGAAAAGTA | AGCCAAGGCT | 120 |

| | |
|---|-----|
| CATTATGCCA AAGGANATAT ACATTTC AAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT | 240 |
| TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA | 300 |
| TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT | 360 |
| GGTGCC | 366 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|---|-----|
| CTGTATAAAC AGAACTCCAC TGCANGAGG AGGCCGGGC CAGGAGAATC TCCGCTTGTC | 60 |
| CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTINC ATTTTTTTAT | 120 |
| TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTTCCC TTNGGCTGGA AAATTTAAAA | 180 |
| ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT | 240 |
| AATTCTTCTT TCCCTCCTTT | 260 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | |
|--|-----|
| ACCTACGTGG GTAAGTTAN AAATGTTATA ATTTTCAGGAA NAGGAACGCA TATAATTGTA | 60 |
| TCTTGCCTAT AATTTTCTAT TTAAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG | 120 |
| GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT | 180 |
| ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCCTA | 240 |
| ATATCCTTCA TGCTTGTAAG GT | 262 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | |
|---|-----|
| ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGCCAA CCCCTGAGCA | 60 |
| CCCCTATCAA CTCCCTTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC | 120 |
| AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA | 180 |
| ANAAATCAGC AGACACAGGT GTAAA | 205 |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TACTGTTTGT | TCTCAGTAAC | AATAAATACA | AAAAGACTGG | TTGTGTTCCG | GCCCCATCCA | 60 |
| ACCACGAAGT | TGATTTCTCT | TGTGTGCAGA | GTGACTGATT | TTAAAGGACA | TGGA | 114 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| ACTAGCCAGC | ACAAAAGGCA | GGGTAGCCTG | AATTGCTTTC | TGCTCTTTAC | ATTTCTTTTA | 60 |
| AAATAAGCAT | TTAGTGCTCA | GTCCCTACTG | AGT | | | 93 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTANGTGCA | GGTGCGCACA | AATATTGTCT | GATATTCCTT | TCATCTTGGA | TTCCATGAGG | 60 |
| TCTTTTGCCC | AGCCTGTGGC | TCTACTGTAG | TAAGTTTCTG | CTGATGAGGA | GCCAGNATGC | 120 |
| CCCCCACTAC | CTTCCCTGAC | GCTCCCCANA | AATCACCCAA | CCTCTGT | | 167 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGGCGTGGT | GCGGAGGGCG | GTACTGACCT | CATTAGTAGG | AGGATGCATT | CTGGCACCCC | 60 |
| GTTCTTCACC | TGTCCCCCAA | TCCTTAAAAG | GCCATACTGC | ATAAAGTCAA | CAACAGATAA | 120 |
| ATGTTTGCTG | AATTAAAGGA | TGGATGAAAA | AAATTAATAA | TGAATTTTGT | CATAATCCAA | 180 |
| TTTTCTCTTT | TATATTCTTA | GAAGAAGTTT | CTTTGAGCCT | ATTAGATCCC | GGGAATCTTT | 240 |
| TAGGTGAGCA | TGATTAGAGA | GCTTGTAGGT | TGCTTTTACA | TATATCTGGC | ATATTTGAGT | 300 |

CTCGTATCAA AACAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | | | | | | |
|-------------------|---------|------------|------------|------------|------------|-----|
| AAAACAAACA AACA | AAAAAAA | ACAATTCTTC | ATTCAGAAAA | ATTATCTTAG | GGACTGATAT | 60 |
| TGGTAATTAT GGTCA | ATTTA | ATWRTT | TKT | GGGGCATTTC | CTTACATTGT | 120 |
| TTAAATGTC TGTGCC | AAAA | TTTTGTATTT | TATTTGGAGA | CTTCTTATCA | AAAGTAATGC | 180 |
| TGCCAAAGGA AGTCTA | AGGA | ATTAGTAGTG | TTCCCMTCAC | TTGTTTGGAG | TGTGCTATTC | 240 |
| TAAAAGATTT TGATTT | CCTG | GAATGACAAT | TATATTTTAA | CTTTGGTGGG | GGAAANAGTT | 300 |
| ATAGGACCAC AGTCTT | CACT | TCTGATACTT | GTAAATTAAT | CTTTTATGTC | ACTTGTTT | 360 |
| ACCATTAAGC TATATG | TTTA | AAA | | | | 383 |

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

| | | | | | | |
|-------------------|------|------------|------------|------------|------------|-----|
| CCCCTGAAGG CTCTTG | TTA | GAAAATAGTA | CAGTTACAAC | CAATAGGAAC | AACAAAAAGA | 60 |
| AAAAGTTTGT GACATT | GTAG | TAGGGAGTGT | GTACCCCTTA | CTCCCCATCA | AAAAAAAAT | 120 |
| GGATACATGG TTAAAG | GATA | RAAGGGCAAT | ATTTTATCAT | ATGTTCTAAA | AGAGAAGGAA | 180 |
| GAGAAAATAC TACTTT | CTCR | AAATGGAAGC | CCTTAAAGGT | GCTTTGATAC | TGAAGGACAC | 240 |
| AAATGTGGCC GTCCAT | CCTC | CTTTARAGTT | GCATGACTTG | GACACGGTAA | CTGTTGCAGT | 300 |
| TTTARACTCM GCATTG | TGAC | | | | | 320 |

CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.